

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:02:32 ; Search time 34.92 seconds  
(without alignments)  
7.778 Million cell updates/sec

Title: US-09-687-267-6  
Perfect score: 12  
Sequence: 1 XXXC 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues  
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_66:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	75.0	3	A22565	R-phycoerythrin al
2	9	75.0	4	I51049	metallothionein-A
3	9	75.0	4	S43959	Ig mu chain V regi
4	9	75.0	4	S5238	pallidipin - assas
5	9	75.0	5	A22565	R-phycoerythrin al
6	9	75.0	5	F22565	R-phycoerythrin ga
7	9	75.0	5	A33882	cadmium-binding pe
8	9	75.0	5	B45525	actin I - malaria
9	9	75.0	5	S65726	hemoglobin, extrac
10	9	75.0	5	JU0355	lipopeptide ws1279
11	9	75.0	6	C22565	R-phycoerythrin be
12	9	75.0	6	I37027	protamine P1 - gor
13	9	75.0	6	I37263	Y protein - human
14	9	75.0	6	S29881	Na+/K+-exchanging
15	9	75.0	6	H48394	glycoprotein compo
16	9	75.0	6	I67345	MHC H2-K-k cell su
17	9	75.0	6	I65546	MHC H2-L antigen -
18	9	75.0	6	PT0652	T-cell receptor be
19	9	75.0	6	F41946	T-cell receptor ga
20	9	75.0	6	I49421	laminin B1 - weste
21	9	75.0	6	I79564	hypothetical TGL3
22	9	75.0	7	PH1408	Ig heavy chain V r
23	9	75.0	7	A58512	venom heptapeptide
24	9	75.0	7	S08606	hypothetical prote
25	9	75.0	7	S38516	mablinin II chain
26	9	75.0	7	B34818	vicillin 57K chain
27	9	75.0	7	B33882	cadmium-binding he
28	9	75.0	7	A34026	acetylcholinestera
29	9	75.0	7	A12016	formylglycinamide

30 9 75.0 7 2 PH1602 Ig H chain V-D-J r  
31 9 75.0 7 2 PH0932 T-cell receptor be  
32 7 4 I56695 hypothetical I2 pr  
33 9 75.0 8 2 PH1407 Ig heavy chain V r  
34 9 75.0 8 2 S59622 metallothionein is  
35 9 75.0 8 2 XGHUEU urine glycopeptide  
36 9 75.0 8 2 A25836 L-serine dehydrata  
37 9 75.0 8 2 PC1002 leucine-tRNA liga  
38 9 75.0 8 2 S19288 acylase - Kluyvera  
39 9 75.0 8 2 A37521 R-phycoerythrin ga  
40 9 75.0 8 2 C61512 variant surface gl  
41 9 75.0 8 2 D61512 variant surface gl  
42 9 75.0 8 2 PH1618 Ig H chain V-D-J r  
43 9 75.0 8 2 PH0803 T-cell receptor al  
44 9 75.0 8 2 I57018 gene Cfr protein  
45 9 75.0 8 2 PH0934 T-cell receptor be

ALIGNMENTS

RESULT 1  
A22565  
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)  
C:Species: Gastroclonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: A22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601  
A:Accession: A22565  
A:Molecule type: protein  
A:Residues: 1-3 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
|  
Db 1 C 1

RESULT 2  
I51049  
metallothionein-A - rainbow trout (fragment)  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I51049  
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.  
Eur. J. Biochem. 230, 344-349, 1995  
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)  
A:Reference number: I51049; MUID:95324545  
A:Accession: I51049  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-4 <OLS>  
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 75.0%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
|  
Db 4 C 4

RESULT 3  
S43959

Ig mu chain V region (clone 13) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
 C:Accession: S43959  
 R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;  
 Nucleic Acids Res. 22, 1389-1393, 1994  
 A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
 A:Reference number: S43956; MUID:94248036  
 A:Accession: S43959  
 A:Molecule type: DNA  
 A:Residues: 1-4 <WAG>  
 C:Keywords: immunoglobulin

Query Match 75.0%; Score 9; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 |  
 Db 2 C 2

RESULT 4  
 S55238  
 pallidipin - assassin bug (fragment)  
 C:Species: Triatoma pallidipennis (assassin bug)  
 C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000  
 C:Accession: S55238  
 R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin  
 Biochem. J. 307, 465-470, 1995  
 A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib  
 A:Reference number: S55238; MUID:95251610  
 A:Accession: S55238  
 A:Molecule type: protein  
 A:Residues: 1-4 <HAE>

Query Match 75.0%; Score 9; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 |  
 Db 3 C 3

RESULT 5  
 B22565  
 R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)  
 C:Species: Gastroclonium coulteri  
 C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
 C:Accession: B22565  
 R:Klotz, A.V.; Glazer, A.N.  
 J. Biol. Chem. 260, 4856-4863, 1985  
 A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
 A:Reference number: A22565; MUID:85182601  
 A:Accession: B22565  
 A:Molecule type: protein  
 A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 |  
 Db 2 C 2

RESULT 6  
 F22565

R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)  
 C:Species: Gastroclonium coulteri  
 C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
 C:Accession: F22565  
 R:Klotz, A.V.; Glazer, A.N.  
 J. Biol. Chem. 260, 4856-4863, 1985  
 A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
 A:Reference number: A22565; MUID:85182601  
 A:Accession: F22565  
 A:Molecule type: protein  
 A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 |  
 Db 3 C 3

RESULT 7  
 A33882  
 cadmium-binding pentapeptide - downy thornapple  
 C:Species: Datura innoxia (downy thornapple)  
 C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 18-Jun-1993  
 C:Accession: A33882  
 R:Jackson, P.J.; Unkefer, C.J.; Dooley, J.A.; Watt, K.; Robinson, N.J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987  
 A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in pla  
 A:Reference number: A94182; MUID:88016144  
 A:Accession: A33882  
 A:Molecule type: protein  
 A:Residues: 1-5 <JAC>

Query Match 75.0%; Score 9; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 |  
 Db 2 C 2

RESULT 8  
 B45525  
 actin I - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C:Date: 03-Jun-1993 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
 C:Accession: B45525  
 R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoen  
 Mol. Biochem. Parasitol. 35, 167-176, 1989  
 A:Title: Stage-specific expression and genomic organization of the actin genes of the  
 A:Reference number: A45525; MUID:89364996  
 A:Accession: B45525  
 A>Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-5 <WES>  
 A:Cross-references: GB:J03988  
 A:Note: the authors translated the codon GAA for residue 3 as Gly  
 C:Comment: The actin I gene contains no introns.

Query Match 75.0%; Score 9; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 |  
 Db 4 C 4

## RESULT 9

S65726  
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)  
C:Species: Lumbricus terrestris (common earthworm)  
C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65726  
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.  
Biochim. Biophys. Acta 1292, 273-280, 1996  
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A:Reference number: S65721; MUID:96176855  
A:Accession: S65726  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <FUS>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 4 C 4

## RESULT 10

JU0355  
lipopeptide WS1279 [validated] - Streptomyces willmorei  
C:Species: Streptomyces willmorei  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: JU0355  
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.  
Chem. Pharm. Bull. 39, 607-611, 1991  
A:Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin  
A:Reference number: JU0355; MUID:91300586  
A:Accession: JU0355  
A:Molecule type: protein  
A:Residues: 1-6 <TSU>  
A>Note: the structure was confirmed by synthesis  
C:Keywords: blocked amino end; lipoprotein  
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental  
F:1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 75.0%; Score 9; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 1 C 1

## RESULT 11

C22565  
R-phycoerythrin beta-1 chain - red alga (Gastrocoulonium coulteri) (fragment)  
C:Species: Gastrocoulonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: C22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601  
A:Accession: C22565  
A:Molecule type: protein  
A:Residues: 1-6 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 4 C 4

## RESULT 12

137027  
protamine P1 - gorilla (fragment)  
C:Species: Gorilla gorilla (gorilla)  
C:Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jul-2000  
C:Accession: I37027  
R:Queralt, R.; Oliva, R.  
Gene 133, 197-204, 1993  
A:Title: Identification of conserved potential regulatory sequences of the protamine-  
A:Reference number: I37013; MUID:94040810  
A:Accession: I37027  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 75.0%; Score 9; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 6 C 6

## RESULT 13

I37263  
Y protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I37263  
R:Waeber, G.; Habener, J.F.  
Endocrinology 131, 2010-2015, 1992  
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternate  
A:Reference number: I37263; MUID:93010891  
A:Accession: I37263  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816  
C:Genetics:  
A:Gene: CREB

Query Match 75.0%; Score 9; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 4 C 4

## RESULT 14

S29881  
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 07-May-1999  
C:Accession: S29881  
R:Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.  
J. Biol. Chem. 260, 3852-3859, 1985  
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases from  
A:Reference number: S29881; MUID:85131201  
A:Accession: S29881  
A:Molecule type: protein  
A:Residues: 1-6 <WAL>  
A:Experimental source: kidney

C;Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;  
F:4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
|  
Db 2 C 2

## RESULT 15

H48394  
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fa  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C:Accession: H48394  
R:Mather, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
II-like sequences.  
A:Reference number: A48394; MUID:93250576  
A:Accession: H48394  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6 <MAT>  
A:Experimental source: milk  
A>Note: sequence extracted from NCBI backbone (NCBIP:131518)  
C:Keywords: glycoprotein

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
|  
Db 6 C 6

Search completed: February 5, 2001, 12:02:33  
Job time: 290 sec



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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:06:02 ; Search time 20.72 Seconds  
(without alignments)  
6.234 Million cell updates/sec

Title: US-09-687-267-6  
Perfect score: 12  
Sequence: 1 XXXX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	9	75.0	8 1 ACT_CARMA	P80709 carcinus ma
2	9	75.0	8 1 GLUR_HUMAN	P02729 homo sapien
3	9	75.0	9 1 CCAP_CARMA	P38556 carcinus ma
4	9	75.0	9 1 CONO_CONGE	P05486 conus geogr
5	9	75.0	9 1 CONO_CONST	P05487 conus stria
6	9	75.0	9 1 DNFI_LOCM1	P16339 locusta mig
7	9	75.0	9 1 ISOT_CYPCA	P42993 cyprinus ca
8	9	75.0	9 1 MGMT_BOVIN	P29177 bos taurus
9	9	75.0	9 1 OXYA_SCYCA	P42996 scyllorhinu
10	9	75.0	9 1 OXYA_SQUAC	P42997 squalus aca
11	9	75.0	9 1 OXYF_SCYCA	P42997 scyllorhinu
12	9	75.0	9 1 OXYT_BUFRE	P42995 bufo regula
13	9	75.0	9 1 OXYT_CYPCA	P23879 cyprinus ca
14	9	75.0	9 1 OXYT_EISFO	P42998 eisenia foe
15	9	75.0	9 1 OXYT_OCTUV	P80027 octopus vul
16	9	75.0	9 1 OXYT_RABIT	P32878 oryctolagus
17	9	75.0	9 1 OXYT_RAJCL	P42994 raja clavav
18	9	75.0	9 1 OXYV_SQUAC	P43000 squalus aca
19	9	75.0	9 1 RSLI_SALTY	O54296 salmonele
20	9	75.0	9 1 SAP_STOVA	P24047 stomopneute
21	9	75.0	9 1 TAL1_PICUA	P17440 pichia jadi
22	9	75.0	9 1 TAL3_PICUA	P17441 pichia jadi
23	9	75.0	10 1 GLEM_HUMAN	P02728 homo sapien
24	9	75.0	10 1 GONZ_CHEPR	P80678 cheilosoma
25	9	75.0	10 1 RCA_PINPS	P81084 pinus pinas
26	9	75.0	12 1 CXAL_CONIM	P50983 conus imper
27	9	75.0	12 1 NO40_LOTUA	O22426 lotus japon
28	9	75.0	12 1 NO40_SESRO	O24369 sesbania ro
29	9	75.0	12 1 NO40_SOYBN	P55960 glycine max
30	9	75.0	12 1 RR16_GINBI	P36207 ginkgo bilo
31	9	75.0	12 1 TAL0_TREME	P01371 tremella me
32	9	75.0	12 1 UR2A_CATCO	P04558 catostomus
33	9	75.0	12 1 UR2B_CATCO	P04559 catostomus

34	9	75.0	12 1	UR2B_CYPCA	P04561 cyprinus ca
35	9	75.0	12 1	UR2_GILMI	P01147 gillichthys
36	9	75.0	12 1	UR2_POLSP	P81022 polyodon sp
37	9	75.0	12 1	UR2_SCYCA	P35490 scyllorhinu
38	9	75.0	12 1	YZPY_ECOLI	P17776 escherichia
39	9	75.0	12 1	ACT7_SOYBN	P15987 glycine max
40	9	75.0	13 1	CXAL_CONST	P15471 conus stria
41	9	75.0	13 1	CXAL2_CONGE	P15120 conus geogr
42	9	75.0	13 1	CXAA_CONST	P28878 conus stria
43	9	75.0	13 1	CXET_CONTE	P81755 conus texti
44	9	75.0	13 1	GER1_HORVU	P28525 hordeum vul
45	9	75.0	13 1	GER2_HORVU	P28526 hordeum vul

ALIGNMENTS

RESULT 1	ACT_CARMA	STANDARD;	PRT;	8 AA.
ID	ACT_CARMA			
AC	P80709;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ACTIN (FRAGMENT).			
OS	Carcinus maenas (Common shore crab) (Green crab).			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;			
OC	Eubrachyura; Portunoidae; Fortunidae; Carcinus.			
RN	[1]			
RP	SEQUENCE.			
RA	Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,			
RA	Baghdassarian D.;			
RT	"A. transaldolase. An enzyme implicated in crab steroidogenesis."			
RL	Endocrine 5:23-32(1996).			
CC	-!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED			
CC	IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED			
CC	IN ALL EUKARYOTIC CELLS.			
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:			
CC	6.8, ITS MW IS: 46 KDA.			
CC	-!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.			
DR	INTERPRO; IPR000279; .			
DR	PROSITE; PS00405; ACTINS_1; PARTIAL.			
DR	PROSITE; PS00432; ACTINS_2; PARTIAL.			
DR	PROSITE; PS01132; ACTINS_ACT-LIKE; PARTIAL.			
KW	Structural protein.			
FT	NON_TER 1 1			
FT	NON_TER 8 8			
SQ	SEQUENCE 8 AA: 976 MW; 1424005AB2CAAE3 CRC64;			

Query Match 75.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4 C 4
Db	2 C 2

RESULT 2	GLUR_HUMAN	STANDARD;	PRT;	8 AA.
ID	GLUR_HUMAN			
ID	P02729;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	URINE GLYCOPETIDE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			

RP SEQUENCE.  
RX MEDLINE-72062338; PubMed-5126885;  
RA Lote C.J., Weiss J.B.;  
RT "Identification in urine of a low-molecular-weight highly polar  
glycopeptide containing cysteinyl-galactose.";  
RL Biochem. J. 123:25P-25P(1971).  
CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE  
IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN  
ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A  
SIMILAR STRUCTURE HAS ALSO BEEN FOUND.  
DR PIR; A03188; XGHUHU.  
KW Glycoprotein.  
FT CARBOHYD  
SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;  
S-LINKED (GAL. -).  
Query Match 75.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 C 4  
DB 1 C 1  
RESULT 3  
CCAP\_CARMA STANDARD; PRT; 9 AA.  
AC P38556;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CARDIOACTIVE PEPTIDE (CCAP).  
OS Manduca sexta (Tobacco hawkmoth) (Green crab),  
OS Carcinus maenas (Common shore crab) (Tobacco hornworm),  
OS Tenebrio molitor (Yellow mealworm), and  
OS Spodoptera eridania (Southern armyworm).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C. MAENAS; TISSUE=PERICARDIAL ORGANS;  
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;  
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
shore crab Carcinus maenas.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=M. SEXTA;  
RX MEDLINE-93050243; PubMed-1426284;  
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;  
RT "Primary structure of a cardioactive neuropeptide from the tobacco  
hawkmoth, Manduca sexta.";  
RL FEBS Lett. 313:165-168(1992).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=T. MOLITOR, AND S. ERIDANIA; TISSUE=HEAD;  
RX MEDLINE-94176032; PubMed-8129851;  
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,  
RA Schooley D.A.;  
RT "Isolation and identification of a cardioactive peptide from Tenebrio  
molitor and Spodoptera eridania.";  
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).  
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.  
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
INTO THE HEMOLYPH.  
DR PIR; A26363; A26363.  
KW Neuropeptide; Amidation.  
FT DISULFID 3 9  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 C 4  
DB 3 C 3  
RESULT 4  
CONO\_CONGE STANDARD; PRT; 9 AA.  
AC P05486;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE LYS-CONOPRESSIN G.  
OS Conus geographus (Geography cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE-88058932; PubMed-3680228;  
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
RA Gray W.R., Olivera B.M.;  
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of  
peptides from Conus geographus and Conus straitus venoms.";  
RL J. Biol. Chem. 262:15821-15824(1987).  
RN [2]  
RP REVIEW.  
RX MEDLINE-89024586; PubMed-3052286;  
RA Gray W.R., Olivera B.M., Cruz L.J.;  
RT "Peptide toxins from venomous Conus snails.";  
RL Annu. Rev. Biochem. 57:665-700(1988).  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR; A28495; A28495.  
DR INTERPRO; IPR000981;  
DR PFAM; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
FT SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;  
AMIDATION.  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 C 4  
DB 1 C 1  
RESULT 5  
CONO\_CONGE STANDARD; PRT; 9 AA.  
AC P05487;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ARG-CONOPRESSIN S.  
OS Conus striatus (Striated cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE-88058932; PubMed-3680228;  
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
RA Gray W.R., Olivera B.M.;  
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of

RT peptides from Conus geographus and Conus straitus venoms.\*;  
 RL J. Biol. Chem. 262:15821-15824 (1987).  
 RN [2]

RP REVIEW.  
 RX MEDLINE=89024586; PubMed=3052286;  
 RA Gray W.R., Olivera B.M., Cruz L.J.;  
 RT "Peptide toxins from venomous Conus snails\*;  
 RL Annu. Rev. Biochem. 57:665-700 (1988).  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR: B28495; B28495.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 DB 1 C 1

RESULT 6  
 DNF1\_LOCFI STANDARD; PRT; 9 AA.  
 AC F16339;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE LOCUPRESSIN (DIURETIC NEUROPEPTIDE F1/F2).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;  
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=SUBESOPHAGEAL GANGLION, AND THORACIC GANGLION;  
 RX MEDLINE=88077077; PubMed=3689410;  
 RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,  
 RA Delaage M., Schooley D.A.;  
 RT "Identification of an arginine vasopressin-like diuretic hormone from  
 RL Locusta migratoria\*;  
 RL Biochem. Biophys. Res. Commun. 149:180-186 (1987).  
 CC -!- FUNCTION: DIURETIC HORMONE.  
 CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR: A29477; A29477.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Neuropeptide; Amidation.  
 FT DISULFID 1 6  
 FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).  
 FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 DB 1 C 1

RESULT 7  
 ISOT\_CYPCA STANDARD; PRT; 9 AA.  
 AC P42993;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE ISOTOCIN.  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=PIUITARY;  
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
 RT "Characterization of neurohypophyseal hormones from a fresh water bony  
 RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea  
 RT water bony fishes\*;  
 RL Comp. Biochem. Physiol. 14:245-254 (1965).  
 CC -!- FUNCTION: ANTIDIURETIC HORMONE.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR: A61364; A61364.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 DB 1 C 1

RESULT 8  
 MGMT\_BOVIN STANDARD; PRT; 9 AA.  
 AC P29177;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) (FRAGMENT).  
 GN MGMT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=THYMUS;  
 RX MEDLINE=90174912; PubMed=2308822;  
 RA Rydberg B., Hall J., Karran P.;  
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA  
 RT methyltransferase\*;  
 RL Nucleic Acids Res. 18:17-21 (1990).  
 CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY  
 CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE  
 CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS  
 CC IRREVERSIBLY INACTIVATED.  
 CC -!- CATALYTIC ACTIVITY: DNA (CONTAINING O6-METHYLGUANINE) + PROTEIN  
 CC L-CYSTEINE = DNA (WITHOUT O6-METHYLGUANINE) + PROTEIN S-METHYL-  
 CC L-CYSTEINE.  
 CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OCT METHYLTRANSFERASE  
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.  
 DR INTERPRO: IPR001497; -.

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DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 3251171A720476047 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 9 C 9

RESULT 9
OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPATOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE
RC TISSUE=PITUITARY;
RA MEDLINE=95062247; PubMed=7972045;
RX Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
isolated from the spotted dogfish (Scyllorhinus caniculus).";
Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -|- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.
CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.
DR INTERPRO; IPR000981; -.
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT MOD_RES 1 6
FT DISULFID 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 10
OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPATOCIN (ASPATOCIN).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;

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RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
isolated from a cartilaginous fish, Squalus acanthias.";
Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
CC C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.
DR INTERPRO; IPR000981; -.
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 11
OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHASVATOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
isolated from the spotted dogfish (Scyllorhinus caniculus).";
Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -|- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.
CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.
DR INTERPRO; IPR000981; -.
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 12
OXYT_BUFRE

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ID OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE SERITOCIN.
OS Bufo regularis (African toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae;
OC Bufo.
RN [1]
RP SEQUENCE.
RC TISSUE-PITUITARY NEUROINTERMEDIATE LOBE;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIN ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO; IPR000981; -.
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 983 MW; 17FF476E5A56D04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
Db 1 C 1

RESULT 13
OXYT_CYPCA STANDARD; PRT; 9 AA.
ID OXYT_CYPCA
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 32, Last annotation update)
DE VASOTOCIN.
OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
RN [1]
RP SEQUENCE.
RC SPECIES=C.CARPIO; TISSUE-PITUITARY;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
fish, the carp (Cyprinus carpio). Comparison with hormones from sea
water bony fishs.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P.MARINUS; TISSUE-PITUITARY;
RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawauchi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
(Petromyzon marinus): Isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; B61364; B61364.
DR PIR; S06375; S06375.
DR INTERPRO; IPR000981; -.
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
Db 1 C 1

RESULT 15
OXYT_OCTVU STANDARD; PRT; 9 AA.
ID OXYT_OCTVU
AC P80027;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CEPHALOTOCIN.
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
RN [1]
RP SEQUENCE.
RC TISSUE-NERVE ENDINGS;

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RX MEDLINE=92270139; PubMed=1589145;  
RA Reich G.;  
RT "A new peptide of the oxytocin/vasopressin family isolated from  
RL nerves of the cephalopod Octopus vulgaris.";  
RL Neurosci. Lett. 134:191-194(1992).  
CC -!- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA  
CAVA.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR INTERPRO; IPR000981; -.  
DR PFAM; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1072 MW; 17FF476EB45409DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
Db 1 C 1

Search completed: February 5, 2001, 12:06:02  
Job time: 279 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2001, 12:05:38 ; Search time 57.72 Seconds  
(without alignments)  
8.123 Million cell updates/sec

Title: US-09-687-267-6  
Perfect score: 12  
Sequence: 1 XXXC 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_15:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_invertebrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9	75.0	6	4 Q08720	Q08720 homo sapien
2	9	75.0	7	2 P70804	P70804 azotobacter
3	9	75.0	7	11 O55184	O55184 rattus norv
4	9	75.0	7	12 Q66113	Q66113 cherry leaf
5	9	75.0	7	12 Q67113	Q67113 influenza a
6	9	75.0	7	12 Q9YVE3	Q9YVE3 human adeno
7	9	75.0	7	12 Q9YIR0	Q9YIR0 human adeno
8	9	75.0	7	12 Q9YIO9	Q9YIO9 human adeno
9	9	75.0	7	13 Q42564	Q42564 fugu rubrip
10	9	75.0	8	2 O32560	O32560 escherichia
11	9	75.0	8	4 Q15888	Q15888 homo sapien
12	9	75.0	8	4 Q15890	Q15890 homo sapien
13	9	75.0	8	4 Q15900	Q15900 homo sapien
14	9	75.0	8	4 Q9Y4X6	Q9Y4X6 homo sapien
15	9	75.0	8	6 O02831	O02831 oryctolagus
16	9	75.0	8	6 Q9TRY3	Q9TRY3 sus sp. ins
17	9	75.0	8	10 Q9SAY7	Q9SAY7 dioscorea t
18	9	75.0	8	11 P70243	P70243 mus musculu
19	9	75.0	8	11 O35835	O35835 rattus norv

20	9	75.0	8	12 Q85562	Q85562 moloney mur
21	9	75.0	8	13 Q90493	Q90493 eopsaltria
22	9	75.0	8	13 Q90498	Q90498 erythrura g
23	9	75.0	8	13 Q91098	Q91098 manorina me
24	9	75.0	9	2 Q47063	Q47063 escherichia
25	9	75.0	9	4 Q15999	Q15999 homo sapien
26	9	75.0	9	4 Q99887	Q99887 homo sapien
27	9	75.0	9	6 Q9XT05	Q9XT05 macropus ru
28	9	75.0	9	6 Q9TUY0	Q9TUY0 monodelphis
29	9	75.0	9	9 Q38340	Q38340 lactococcus
30	9	75.0	9	11 Q9QZ88	Q9QZ88 mus musculu
31	9	75.0	9	11 P97889	P97889 rattus norv
32	9	75.0	9	12 Q69473	Q69473 human herpe
33	9	75.0	9	12 O12096	O12096 caprine art
34	9	75.0	9	12 O12098	O12098 caprine art
35	9	75.0	9	12 O12100	O12100 caprine art
36	9	75.0	9	12 O12102	O12102 caprine art
37	9	75.0	9	12 O12104	O12104 caprine art
38	9	75.0	9	12 Q90350	Q90350 hepatitis g
39	9	75.0	10	2 Q50032	Q50032 mycobacteri
40	9	75.0	10	2 Q47475	Q47475 escherichia
41	9	75.0	10	2 Q48469	Q48469 klebsiella
42	9	75.0	10	2 Q9K343	Q9K343 escherichia
43	9	75.0	10	3 Q9UW2	Q9UW2 schizophyll
44	9	75.0	10	4 Q13318	Q13318 homo sapien
45	9	75.0	10	4 Q9UN90	Q9UN90 homo sapien

ALIGNMENTS

RESULT 1

Q08720 PRELIMINARY; PRT; 6 AA.

AC Q08720; PRELIMINARY; PRT; 6 AA.

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE Y PROTEIN (FRAGMENT).

GN CREB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93010691; PubMed=1396344;

RA Waeber G., Habener J.F.;

RT "Novel testis germ cell-specific transcript of the CREB gene contains an alternatively spliced exon with multiple in-frame stop codons.";

RL Endocrinology 131:2010-2015(1992).

DR EMBL; X68994; CAA48780.1; -.

FT NON\_TER 1 1

FT NON\_TER 6 6

SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4

Db 4 C 4

RESULT 2

ID P70804 PRELIMINARY; PRT; 7 AA.

AC P70804; PRELIMINARY; PRT; 7 AA.

DT 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE ALGG GENE (FRAGMENT).  
GN ALGT.  
OS Azotobacter vinelandii.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Azotobacter.  
OX NCBI\_TaxID=354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E.  
RX MEDLINE=96427318; PubMed=8830682;  
RA Rehm B.H.A.; Ertesvag H.; Valla S.;  
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algC) is  
RT part of an alg gene cluster physically organized in a manner similar  
RT to that in Pseudomonas aeruginosa";  
RL J. Bacteriol. 178:5884-5889(1996).  
DR EMBL; X87973; CAA61230.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
|  
Db 1 C 1

RESULT 3  
O55184 PRELIMINARY; PRT; 7 AA.  
AC O55184;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE ORPHAN RECEPTOR TR4-NS (FRAGMENT).  
GN TR4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96198747; PubMed=8612486;  
RA Yoshikawa T.; Makino S.; Gao X.M.; Xing G.Q.; Chuang D.M.;  
RA Detera-Wadleigh S.D.;  
RT "Splice variants of rat TR4 orphan receptor: differential expression  
RT of novel sequences in the 5'-untranslated region and C-terminal  
RT domain";  
RL Endocrinology 137:1562-1571(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96299786; PubMed=8661150;  
RA Yoshikawa T.; Dupont B.R.; Leach R.J.; Detera-Wadleigh S.D.;  
RT "New variants of the human and rat nuclear hormone receptor, TR4:  
RT expression and chromosomal localization of the human gene";  
RL Genomics 35:361-366(1996).  
DR EMBL; U59454; AAB91433.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 75.0%; Score 9; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
|  
Db 3 C 3

RESULT 4

Q66113 PRELIMINARY; PRT; 7 AA.  
ID Q66113;  
AC Q66113;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE C-TERMINUS OF THE VIRAL REPLICASE (FRAGMENT).  
OS cherry leaf roll virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;  
OC Nepovirus.  
OX NCBI\_TaxID=12615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WALNUT;  
RA Borja M.;  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WALNUT;  
RX MEDLINE=96124520; PubMed=8560786;  
RA Borja M.; Sanchez F.; Rowhani A.; Bruening G.; Ponz F.;  
RT "Long, nearly identical untranslated sequences at the 3' terminal  
RT regions of the genomic RNAs of cherry leafroll virus (walnut  
RT strain)";  
RL Virus Genes 10:245-252(1995).  
DR EMBL; Z34265; CAA84019.1; -.  
KW Repeat.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
|  
Db 4 C 4

RESULT 5  
Q67113 PRELIMINARY; PRT; 7 AA.  
ID Q67113;  
AC Q67113;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE (UDORN/72) HEMAGGLUTININ (SEG 4) CDNA, 3' END (FRAGMENT).  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81001892; PubMed=7407922;  
RA Dhar R.; Chanock R.M.; Lai C.J.;  
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza  
RT viral mRNA deduced from cloned complete genomic sequences";  
RL Cell 21:495-500(1980).  
DR EMBL; M25045; AAA43202.1; -.  
KW Hemagglutinin.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 834 MW; 505EB0544EA40030 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
|  
Db 3 C 3



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RESULT 6
QYI03
ID Q9YVE3 PRELIMINARY; PRT; 7 AA.
AC Q9YVE3;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GOMEN;
RA Crawford-Miksz L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065065; AAD03662.1; -.
DR EMBL; AF065065; AAD03662.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
Db 6 C 6

RESULT 7
QYI03
ID Q9YI03 PRELIMINARY; PRT; 7 AA.
AC Q9YI03;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7a.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=85755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-KN T96-0620, S-1058, CL 68578;
RA Crawford-Miksz L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065068; AAD03668.1; -.
DR EMBL; AF065068; AAD03668.1; -.
DR EMBL; AF065067; AAD03666.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
Db 6 C 6

RESULT 8
QYI09
ID Q9YI09 PRELIMINARY; PRT; 7 AA.
AC Q9YI09;

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DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 4.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Z-G 95-873, RI-67, 55142;
RA Crawford-Miksz L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03659.1; -.
DR EMBL; AF065062; AAD03653.1; -.
DR EMBL; AF065063; AAD03656.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
Db 6 C 6

RESULT 9
O42564 PRELIMINARY; PRT; 7 AA.
ID O42564;
AC O42564;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT (FRAGMENT).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
DR EMBL; U97673; AAB80916.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B7EA2C73772A0 CRC64;

Query Match 75.0%; Score 9; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
Db 5 C 5

RESULT 10
O32560 PRELIMINARY; PRT; 8 AA.
ID O32560;
AC O32560;
DT 01-JAN-1998 (TRENBLrel. 05, Created)

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DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
GN PROPIONATE KINASE (FRAGMENT).  
OS TDCD.  
OC Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OX NCBI\_TaxID=562;  
RP SEQUENCE FROM N.A.  
RA STRAIN=W3110;  
RC Hesslinger C., Sawers G.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W3110;  
RA Hesslinger C., Fairhurst S.A., Sawers G.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ001620; CAA04875.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
DB 6 C 6

RESULT 11  
Q15888  
ID Q15888 PRELIMINARY; PRT; 8 AA.  
AC Q15888;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
DE (CLONE XP15H8A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32069; AAA73878.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB580763 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
DB 5 C 5

RESULT 12  
Q15890  
ID Q15890 PRELIMINARY; PRT; 8 AA.  
AC Q15890;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)

DE (CLONE XP19G12A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32083; AAA73880.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
DB 4 C 4

RESULT 13  
Q15900  
ID Q15900 PRELIMINARY; PRT; 8 AA.  
AC Q15900;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
DE (CLONE XP7B11A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32079; AAA73890.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAEB1 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
DB 2 C 2

RESULT 14  
Q9Y4X6  
ID Q9Y4X6 PRELIMINARY; PRT; 8 AA.  
AC Q9Y4X6;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE NUCLEAR LIM INTERACTOR (FRAGMENT).  
GN NLI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
RA Schroth A., Bodem J., Royer-Pokora B.;
RT "Genomic structure, alternative transcripts and chromosomal
RT localization of the human LIM domain binding protein 1 gene
RT LDB1/NLI.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243097; CAB45408.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 767 MW; EE6EBDEB862D5B6 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
Db 5 C 5

RESULT 15
002831 PRELIMINARY; PRT; 8 AA.
AC O02831;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; Pubmed=8783186;
RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 75.0%; Score 9; DB 6; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
Db 4 C 4
```

Search completed: February 5, 2001, 12:05:38  
Job time: 289 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	9	75.0	3	2	P10301	Sequence which cor	
2	9	75.0	3	10	P90982	Binding receptor w	
3	9	75.0	3	10	P31650	Synthetic peptide	
4	9	75.0	3	14	R34022	Metal trapping pep	
5	9	75.0	3	14	R34023	Metal trapping pep	
6	9	75.0	3	15	R51439	IGF-1 analogue N-t	
7	9	75.0	3	15	R51440	IGF-1 analogue N-t	
8	9	75.0	3	15	R51441	IGF-1 analogue N-t	
9	9	75.0	3	18	W19847	Human interleukin	
10	9	75.0	3	19	W56231	Anti-inflammatory	
11	9	75.0	3	19	W56211	Anti-inflammatory	
12	9	75.0	3	19	W56200	Anti-inflammatory	

XX  
DR WPI; 1981-53498D/30 (53498D).

PT Cysteine peptide(s) with antidiabetic activity - contg. fragments  
 PT Of insulin A and B chains

XX Claim 1; Page 10; 11pp; German.

XX The inventors claim the prepn. of new cysteine peptides with insulin-  
 CC like activity. The new peptides comprise a sequence with corresp. to  
 CC a central portion of the insulin B chain (esp. B15-27) and a  
 CC cysteine-contg. peptide with an AA sequence corresp. to a terminal  
 CC portion of the insulin A chain (esp. A1-7). The new cysteine  
 CC peptides are antidiabetic agents with appreciable insulin activity  
 CC (lower than that of insulin itself) and low antigenic activity.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
 I  
 Db 2 c 2

RESULT 2

P90982  
 ID P90982 standard; peptide; 3 AA.

AC P90982;

XX 06-JUN-1990 (first entry)

DE Binding receptor with selectivity for a target ligand, borne by  
 DE an article for inactivating toxic materials.

KW Toxic material; inactivator; organophosphorous cpds.; nerve poison;  
 KW pesticide; decontaminant; military.

XX WO8902920-A.

XX 06-APR-1989.

XX 04-OCT-1988; 88WO-US03422.

XX 05-OCT-1987; 87US-0105312.

XX (LITT ) LITTLE AD INC.

XX Taylor RF;

XX WPI; 1989-114395/15.

PT Article for inactivating toxic materials, eg organo:phosphorous cpds. -  
 PT comprises solid carrier bearing target ligand binding receptor  
 PT and ligand-degrading receptor, pref. enzyme

XX Claim 7a; page 42; 57pp; English.

XX The article for inactivating a toxic material comprises a solid carrier  
 CC bearing a first receptor which binds the target ligand and a second  
 CC receptor which degrades the target ligand. This synthetic peptide is  
 CC a preferred first receptor. The article may be used for covering  
 CC surfaces to protect or decontaminate the surface. The article is esp. for  
 CC degrading toxic organic cpds., esp. organophosphorous cpds., (eg  
 CC pesticides and nerve poisons, bacteria and viruses, in environmental,  
 CC chemical, military and industrial settings.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
 I  
 Db 2 c 2

RESULT 3

P91660  
 ID P91660 standard; protein; 3 AA.

XX P91660;

XX 29-JUN-1990 (first entry)

XX Synthetic peptide corresp. to residues 12-14 of naturally occurring  
 DE epidermal growth factor (EGF).

XX Epidermal growth factor; angiogenesis; synthetic peptide.

XX Key : Location/Qualifiers

FT Misc-difference 1

FT : /label=OTHER

FT /note="H-Gly"

FT Misc-difference 3

FT /label=OTHER

FT /note="(aceto amido methyl) NH2-Cys"

XX WO8901489-A.

XX 23-FEB-1989.

XX 10-AUG-1988; 88WO-AU00300.

XX 10-AUG-1987; 87AU-0003629.

XX (CSIR ) COMMONWEALTH SCIENT ORG.

XX McAuslan BR;

XX WPI; 1989-068852/09.

PT Synthetic peptide active in stimulating angiogenesis -  
 PT has sequences corresponding to amino acid sequences occurring in  
 PT epidermal growth factor.

XX Claim 3; page 10; 11pp; English.

XX The inventors claim synthetic peptides which correspond to sequences  
 CC occurring in EGF, but excluding EGF. The peptides are angiogenic  
 CC and have corresp. applications, eg for the healing of wounds and  
 CC burns. Their relative shortness means that they pose fewer synthesis  
 CC problems than the entire EGF molecule. They can be admin. singly or  
 CC association with each other or in association with an angiogenic  
 CC stimulator.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
 I  
 Db 3 c 3

RESULT 4

R34022  
 ID R34022 standard; peptide; 3 AA.

XX R34022;

XX 19-MAY-1993 (first entry)  
XX Metal trapping peptide intermediate.  
XX Electrostatic interaction; metalloprotein; binding site;  
XX protecting group.  
XX Synthetic.  
XX Key Location/Qualifiers  
XX Modified-site 1 /note= "Boc protected"  
XX Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH  
XX Modified-site 3 /note= "OME protected"  
XX JP04346999-A.  
XX 02-DEC-1992.  
XX 24-MAY-1991; 91JP-0120196.  
XX 24-MAY-1991; 91JP-0120196.  
XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.  
XX WPI; 1993-021449/03.  
XX New acyclic peptide with metal trapping activity - exhibits in  
XX vivo metal transporting action and can be used as drug,  
XX diagnostic agent or functional material  
XX Claim 3; Page 2; 9pp; Japanese.  
XX The acyclic peptide (see R31340) with metal trapping activity may be  
XX produced by fragment condensation using the peptide fragments given in  
XX R34022-29.  
XX Sequence 3 AA;  
SQ  
Query Match 75.0%; Score 9; DB 14; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 C 1  
Db 2 C 2  
RESULT 5  
R34023  
ID R34023 standard; peptide; 3 AA.  
XX  
AC R34023;  
XX  
XX 19-MAY-1993 (first entry)  
XX Metal trapping peptide intermediate.  
XX Electrostatic interaction; metalloprotein; binding site;  
XX protecting group.  
XX Synthetic.  
XX Key Location/Qualifiers  
XX Modified-site 1 /note= "HCl.H-Val"  
XX Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH

FT Modified-site 3 /note= "OME protected"  
FT  
XX  
XX JP04346999-A.  
XX  
XX 02-DEC-1992.  
XX  
XX 24-MAY-1991; 91JP-0120196.  
XX  
XX 24-MAY-1991; 91JP-0120196.  
XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.  
XX WPI; 1993-021449/03.  
XX New acyclic peptide with metal trapping activity - exhibits in  
XX vivo metal transporting action and can be used as drug,  
XX diagnostic agent or functional material  
XX Claim 3; Page 2; 9pp; Japanese.  
XX The acyclic peptide (see R31340) with metal trapping activity may be  
XX produced by fragment condensation using the peptide fragments given in  
XX R34022-29.  
XX Sequence 3 AA;  
SQ  
Query Match 75.0%; Score 9; DB 14; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 C 1  
Db 2 C 2  
RESULT 6  
R51439  
ID R51439 standard; peptide; 3 AA.  
XX  
AC R51439;  
XX  
XX 27-OCT-1994 (first entry)  
XX IGF-1 analogue N-terminal.  
XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;  
XX in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.  
XX Homo sapiens.  
XX  
XX WO9406445-A.  
XX  
XX 31-MAR-1994.  
XX  
XX 02-SEP-1993; 93WO-US08279.  
XX  
XX 17-SEP-1992; 92US-0947035.  
XX (EMBR-) EMBREX INC.  
XX (GROP-) GROPEP PTY LTD.  
XX (USDA ) US SEC OF AGRIC.  
XX Ballard FJ, Francis GL, McMurry JP, Phelps PV;  
XX Walton PE;  
XX WPI; 1994-118144/14.  
XX Increasing growth of birds - with insulin-like growth factor  
XX delivered to the egg before hatching esp. for increasing wt. gain  
XX in chickens.

XX Claim 6; Page 37; 45pp; English.  
 XX Growth of birds is increased by (a) admin. to the bird, in ovo,  
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;  
 CC (b) incubating to hatch and (c) growing the birds for at least 3  
 CC weeks after hatch.  
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or  
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,  
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced  
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal  
 CC given in R51439-49.  
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced  
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent  
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.  
 CC comprises the N-terminal given in R51450-53.  
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human  
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid  
 CC N-terminal extension.  
 XX Sequence 3 AA;  
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
 DB 3 C 3

RESULT 7  
 R51440  
 ID R51440 standard; peptide; 3 AA.  
 XX  
 AC R51440;  
 XX  
 DT 27-OCT-1994 (first entry)  
 XX  
 DE IGF-1 analogue N-terminal.  
 XX  
 KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;  
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9406445-A.  
 XX  
 PD 31-MAR-1994.  
 XX  
 PF 02-SEP-1993; 93WO-US08279.  
 XX  
 PR 17-SEP-1992; 92US-0947035.  
 XX  
 PA (EMBR-) EMBREX INC.  
 PA (GROP-) GROPEP PTY LTD.  
 PA (USDA) US SEC OF AGRIC.  
 XX  
 PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;  
 PI Walton PE;  
 XX  
 DR WPI; 1994-118144/14.  
 XX  
 PT Increasing growth of birds - with insulin-like growth factor  
 PT delivered to the egg before hatching esp. for increasing wt. gain  
 PT in chickens.  
 XX  
 PS Claim 6; Page 37; 45pp; English.  
 XX  
 CC Growth of birds is increased by (a) admin. to the bird, in ovo,  
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;  
 CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.  
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or  
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,  
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced  
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal  
 CC given in R51439-49.  
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced  
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent  
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.  
 CC comprises the N-terminal given in R51450-53.  
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human  
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid  
 CC N-terminal extension.  
 XX Sequence 3 AA;  
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
 DB 3 C 3

RESULT 8  
 R51441  
 ID R51441 standard; peptide; 3 AA.  
 XX  
 AC R51441;  
 XX  
 DT 27-OCT-1994 (first entry)  
 XX  
 DE IGF-1 analogue N-terminal.  
 XX  
 KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;  
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9406445-A.  
 XX  
 PD 31-MAR-1994.  
 XX  
 PF 02-SEP-1993; 93WO-US08279.  
 XX  
 PR 17-SEP-1992; 92US-0947035.  
 XX  
 PA (EMBR-) EMBREX INC.  
 PA (GROP-) GROPEP PTY LTD.  
 PA (USDA) US SEC OF AGRIC.  
 XX  
 PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;  
 PI Walton PE;  
 XX  
 DR WPI; 1994-118144/14.  
 XX  
 PT Increasing growth of birds - with insulin-like growth factor  
 PT delivered to the egg before hatching esp. for increasing wt. gain  
 PT in chickens.  
 XX  
 PS Claim 6; Page 37; 45pp; English.  
 XX  
 CC Growth of birds is increased by (a) admin. to the bird, in ovo,  
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;  
 CC (b) incubating to hatch and (c) growing the birds for at least 3  
 CC weeks after hatch.  
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or  
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,  
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced  
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal  
 CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced  
 CC by Gly, Gln, Ieu, Arg or Lys, partic. Gly and the Thr normally adjacent  
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.  
 CC comprises the N-terminal given in R51450-53.  
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human  
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid  
 CC N-terminal extension.  
 XX  
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 15; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1

Db 3 C 3

RESULT 9

W19847  
 ID W19847 standard; Peptide; 3 AA.

XX

AC W19847;

XX

XX 23-SEP-1997 (first entry)

DT

XX

DE Human interleukin-12 p40 subunit N-terminal peptide.

XX

XX Interleukin-12; Fc gamma-1; immunosuppressive; autoimmune disease;  
 KW graft rejection; toxic shock; therapy.

XX

OS Homo sapiens.

XX

PN WO9720062-A1.

XX

XX 05-JUN-1997.

XX

PF 02-DEC-1996; 96WO-US19181.

XX

PR 01-DEC-1995; 95US-0565856.

XX

PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX

PA (UYMA-) UNIV MASSACHUSETTS.

XX

PI Steel AW, Strom TB;

XX

DR WPI; 1997-310615/28.

XX

DR N-PSDB; T72095-96.

XX

PT Fusion protein containing interleukin-12 p40 sub-unit - has

XX

PT increased stability, used to inhibit graft rejection, or treat

XX

PT autoimmune disease and endotoxin-induced shock

XX

PS Example; Fig 2; 36pp; English.

XX

CC A peptide (W19847) comprises the three N-terminal amino acid  
 CC residues of human interleukin-12 (IL-12) p40 subunit. It is  
 CC encoded both by native human p40 cDNA (T72096) and by a primer  
 CC (T72095), based on the native sequence. PCR amplification has  
 CC been used to amplify p40 cDNA. A fusion protein comprising the  
 CC p40 subunit and human Fc gamma-1 (see also W19853) was expressed  
 CC in E. coli. This fusion protein has a longer in vivo half-life  
 CC than native p40 and can be used as an immunosuppressive (e.g. to  
 CC treat autoimmune diseases or to inhibit graft rejection) or to  
 CC treat or prevent endotoxin-induced shock.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 18; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 C 1  
 Db 2 C 2

RESULT 10

W56231  
 ID W56231 standard; peptide; 3 AA.

XX

AC W56231;

XX

DT 20-JUL-1998 (first entry)

XX

DE Anti-inflammatory tripeptide.

XX

KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;  
 KW T-cell inhibitory activity; adherence; extracellular matrix;  
 KW up-regulation; fas receptor expression; inflammation.

XX

OS Synthetic.

XX

PN WO9809985-A2.

XX

PD 12-MAR-1998.

XX

PF 03-SEP-1997; 97WO-IL00295.

XX

PR 28-MAY-1997; 97US-0864301.

XX

PR 03-SEP-1996; 96US-0025376.

XX

PR 20-NOV-1996; 96US-0753141.

XX

PA (YEDA ) YEDA RES &amp; DEV CO LTD.

XX

PI Beserman P, Eisenbachschwartz M, Hirschberg DL;

XX

WPI; 1998-193550/17.

XX

XX Anti-inflammatory peptides and derivatives - used for treating, e.g.

XX arthritis, ulcerative colitis, auto-immune disease, allergy asthma,

XX shock, HIV infection, transplant rejection or Alzheimer's disease

XX

PS Claim 7; Page 35; 42pp; English.

XX

XX W56171-248 represent anti-inflammatory tripeptides of the invention.

XX

CC They are derived from the formulae:

XX

CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where

XX

CC Xaa = any amino acid residue.

XX

CC Cyclic derivatives of the peptides also function as anti-inflammatory  
 CC agents. The peptides can be covalently linked to one another either  
 CC directly or through a spacer. The peptides and their derivatives have  
 CC macrophage inhibitory and T-cell inhibitory activity and thus,  
 CC anti-inflammatory activity. The peptides and compositions have  
 CC anti-immune activity, i.e. inhibitory effects against a cellular and  
 CC humoral immune response, including a response not associated with  
 CC inflammation. The peptides also inhibit the ability of macrophages and  
 CC T-cells to adhere to extracellular matrix components and fibronectin, as  
 CC well as up-regulated fas receptor expression in T-cells. They can be used  
 CC to inhibit unwanted immune reaction and inflammation.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1

Db 3 C 3



```

RESULT 11
ID W56211 standard; peptide; 3 AA.
XX AC W56211;
XX DT 20-JUL-1998 (first entry)
XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
XX KW T-cell inhibitory activity; adherence; extracellular matrix;
XX KW up-regulation; fas receptor expression; inflammation.
XX OS Synthetic.
XX PN W09809985-A2.
XX PD 12-MAR-1998.
XX PF 03-SEP-1997; 97WO-IL00295.
XX PR 28-MAY-1997; 97US-0864301.
XX PR 03-SEP-1996; 96US-0025376.
XX PR 20-NOV-1996; 96US-0753141.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX WPI; 1998-193550/17.
XX DT Anti-inflammatory peptides and derivatives - used for treating, e.g.
XX DT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
XX DT shock, HIV infection, transplant rejection or Alzheimer's disease
XX PS Claim 6; Page 35; 42pp; English.
XX W56171-248 represent anti-inflammatory tripeptides of the invention.
XX CC They are derived from the formulae:
XX CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
XX CC Xaa = any amino acid residue.
XX CC Cyclic derivatives of the peptides also function as anti-inflammatory
XX CC agents. The peptides can be covalently linked to one another either
XX CC directly or through a spacer. The peptides and their derivatives have
XX CC macrophage inhibitory and T-cell inhibitory activity and thus,
XX CC anti-inflammatory activity. The peptides and compositions have
XX CC anti-immune activity, i.e. inhibitory effects against a cellular and
XX CC humoral immune response, including a response not associated with
XX CC inflammation. The peptides also inhibit the ability of macrophages and
XX CC T-cells to adhere to extracellular matrix components and fibronectin, as
XX CC well as up-regulated fas receptor expression in T-cells. They can be used
XX CC to inhibit unwanted immune reaction and inflammation.
XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 12
ID W56200 standard; peptide; 3 AA.
XX AC W56200;
XX DT 20-JUL-1998 (first entry)

```

```

XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
XX KW T-cell inhibitory activity; adherence; extracellular matrix;
XX KW up-regulation; fas receptor expression; inflammation.
XX OS Synthetic.
XX PN W09809985-A2.
XX PD 12-MAR-1998.
XX PF 03-SEP-1997; 97WO-IL00295.
XX PR 28-MAY-1997; 97US-0864301.
XX PR 03-SEP-1996; 96US-0025376.
XX PR 20-NOV-1996; 96US-0753141.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX WPI; 1998-193550/17.
XX DT Anti-inflammatory peptides and derivatives - used for treating, e.g.
XX DT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
XX DT shock, HIV infection, transplant rejection or Alzheimer's disease
XX PS Claim 5; Page 34; 42pp; English.
XX W56171-248 represent anti-inflammatory tripeptides of the invention.
XX CC They are derived from the formulae:
XX CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
XX CC Xaa = any amino acid residue.
XX CC Cyclic derivatives of the peptides also function as anti-inflammatory
XX CC agents. The peptides can be covalently linked to one another either
XX CC directly or through a spacer. The peptides and their derivatives have
XX CC macrophage inhibitory and T-cell inhibitory activity and thus,
XX CC anti-inflammatory activity. The peptides and compositions have
XX CC anti-immune activity, i.e. inhibitory effects against a cellular and
XX CC humoral immune response, including a response not associated with
XX CC inflammation. The peptides also inhibit the ability of macrophages and
XX CC T-cells to adhere to extracellular matrix components and fibronectin, as
XX CC well as up-regulated fas receptor expression in T-cells. They can be used
XX CC to inhibit unwanted immune reaction and inflammation.
XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 3 C 3

RESULT 13
ID W56172 standard; peptide; 3 AA.
XX AC W56172;
XX DT 20-JUL-1998 (first entry)
XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
XX KW T-cell inhibitory activity; adherence; extracellular matrix;
XX KW up-regulation; fas receptor expression; inflammation.
XX

```

OS Synthetic.  
PN W09809985-A2.  
XX  
PD 12-MAR-1998.  
XX  
PF 03-SEP-1997; 97WO-IL00295.  
XX  
XX 28-MAY-1997; 97US-0864301.  
PR 03-SEP-1996; 96US-0025376.  
PR 20-NOV-1996; 96US-0753141.  
XX  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Beserman P, Eisenbachschwartz M, Hirschberg DL;  
XX  
XX WPI; 1998-193350/17.  
XX  
XX Anti-inflammatory peptides and derivatives - used for treating, e.g.  
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,  
PT shock, HIV infection, transplant rejection or Alzheimer's disease  
XX  
PS Claim 3; Page 34; 42pp; English.  
XX  
CC W56171-248 represent anti-inflammatory tripeptides of the invention.  
CC They are derived from the formulae:  
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where  
CC Xaa = any amino acid residue.  
CC Cyclic derivatives of the peptides also function as anti-inflammatory  
CC agents. The peptides can be covalently linked to one another either  
CC directly or through a spacer. The peptides and their derivatives have  
CC macrophage inhibitory and T-cell inhibitory activity and thus,  
CC anti-inflammatory activity. The peptides and compositions have  
CC anti-immune activity, i.e. inhibitory effects against a cellular and  
CC humoral immune response, including a response not associated with  
CC inflammation. The peptides also inhibit the ability of macrophages and  
CC T-cells to adhere to extracellular matrix components and fibronectin, as  
CC well as up-regulated fas receptor expression in T-cells. They can be used  
CC to inhibit unwanted immune reaction and inflammation.  
XX  
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 1 C 1

RESULT 14  
W88037  
ID W88037 standard; peptide; 3 AA.  
XX  
AC W88037;  
XX  
DT 09-APR-1999 (first entry)  
XX  
DE Peptide used in the hair composition of the invention.  
XX  
KW Hair; styling; wave.  
XX  
XX Synthetic.  
OS  
XX  
PN JP11012138-A.  
XX  
XX 19-JAN-1999.  
PD  
XX  
PF 18-JUN-1997; 97JP-0161657.  
XX

PR 18-JUN-1997; 97JP-0161657.  
XX  
PA (LIOY ) LION CORP.  
XX  
XX WPI; 1999-148442/13.  
XX  
XX New composition for hair - comprises oligopeptide having more than 2  
PT cysteine residues and reducing agent  
XX  
PS Example 2; Page 6; 17pp; Japanese.  
XX  
CC Peptides W88033-39 are used in the hair composition of the invention.  
CC The specification describes a hair composition that comprises at  
CC least one oligopeptide having more than two cysteine residues and more  
CC than three amino acid residues of the same kind (except cysteine) and a  
CC reducing agent. The composition is useful for styling hair to take  
CC various shapes and waves safely and effectively.  
XX  
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 20; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 1 C 1

RESULT 15  
Y51896  
ID Y51896 standard; peptide; 3 AA.  
XX  
AC Y51896;  
XX  
DT 16-JUN-2000 (first entry)  
XX  
DE Biostatin TT232 synthesising peptide 1.  
XX  
KW Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor;  
KW cellular proliferation inhibition; somatostatin; antitumor.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT Modified-site 2 /note= "TFA\*Lys(2)"  
FT Modified-site 3 /note= "Cys(Acm)"  
FT Modified-site 3 /note= "Thr(tBu) with C-terminal amide group"  
XX  
PN W0200011032-A2.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-EP06131.  
XX  
PR 20-AUG-1998; 98WO-EP05306.  
XX  
PA (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.  
XX  
PI Braum G, Lifferth A, Birr C;  
XX  
XX WPI; 2000-224663/19.  
XX  
XX Biostatin preparation in high yield by solid synthesis, including  
PT closure of disulfide bridge before cleavage from support, useful as  
PT antitumor agent  
XX  
XX Example 4; Page 23; 33pp; German.  
XX

CC This invention describes a novel method for the solid phase (SP)  
 CC synthesis of biostatin (RT 232) (I) which includes closing the disulfide  
 CC bridge by oxidation of the completely or partially constructed peptide  
 CC while still bonded to the solid phase. The products of the invention have  
 CC cytostatic activity and are tyrosine kinase inhibitors. (I) inhibits the  
 CC tyrosine kinase activity of various human stomach cancer cell lines and  
 CC thus inhibits cellular proliferation. The heptapeptide (I) described in  
 CC the invention is a somatostatin analog which shows strong antitumor  
 CC activity in vitro and in vivo. The SP synthesis method gives (I) is more  
 CC easily and in markedly higher yield than by the method of EP505680, in  
 CC which the cyclization is carried out after cleaving the peptide from the  
 CC resin. The solution method is also a simple synthesis of (I) in high  
 CC yield; typically the tert-butyl-protected precursor can be oxidized in  
 CC a yield of 70-80%. Y51896-Y51900 represent peptides used in the  
 CC synthesis of biostatin RT232 described in the method of the invention.

XX  
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 21; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
 Db 2 c 2

Search completed: February 5, 2001, 12:01:19  
 Job time: 366 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 11:56:18 ; Search time 30.91 Seconds  
(without alignments)  
2.324 Million cell updates/sec

Title: us-09-687-267-1

Perfect score: 12

Sequence: 1 CXXX 4

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/iaa/6\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/iaa/PCBUS\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	75.0	2	1	US-07-791-213D-23
2	9	75.0	2	1	US-07-791-213D-39
3	9	75.0	2	1	US-08-133-804-9
4	9	75.0	2	1	US-08-354-240A-12
5	9	75.0	2	1	US-08-461-838-9
6	9	75.0	2	1	US-08-293-150A-23
7	9	75.0	2	1	US-08-293-150A-39
8	9	75.0	2	2	US-08-461-386-9
9	9	75.0	2	2	US-08-465-380-307
10	9	75.0	2	2	US-08-486-397-307
11	9	75.0	2	2	US-08-486-399-307
12	9	75.0	2	2	US-08-461-965-307
13	9	75.0	2	2	US-08-634-641-307
14	9	75.0	2	2	US-08-818-253-52
15	9	75.0	2	3	US-09-249-471-307
16	9	75.0	2	3	US-09-249-472-307
17	9	75.0	2	3	US-09-249-451-307
18	9	75.0	2	3	US-08-809-455-307
19	9	75.0	2	3	US-09-249-461-307
20	9	75.0	2	3	US-09-249-448-307
21	9	75.0	3	1	US-07-791-213D-22
22	9	75.0	3	1	US-07-791-213D-38
23	9	75.0	3	1	US-07-945-982-2
24	9	75.0	3	1	US-07-945-982-8
25	9	75.0	3	1	US-07-947-035-3
26	9	75.0	3	1	US-07-947-035-4
27	9	75.0	3	1	US-07-947-035-5
28	9	75.0	3	1	US-08-285-443-4

29	9	75.0	3	1	US-08-079-812-31	Sequence 31, Appl
30	9	75.0	3	1	US-08-122-510-11	Sequence 11, Appl
31	9	75.0	3	1	US-08-122-510-12	Sequence 12, Appl
32	9	75.0	3	1	US-08-122-510-13	Sequence 13, Appl
33	9	75.0	3	1	US-07-789-913-26	Sequence 26, Appl
34	9	75.0	3	1	US-08-371-930-4	Sequence 4, Appl
35	9	75.0	3	1	US-08-049-794-26	Sequence 26, Appl
36	9	75.0	3	1	US-08-372-455-2	Sequence 2, Appl
37	9	75.0	3	1	US-08-372-455-8	Sequence 8, Appl
38	9	75.0	3	1	US-08-321-585A-1	Sequence 1, Appl
39	9	75.0	3	1	US-08-321-585A-2	Sequence 2, Appl
40	9	75.0	3	1	US-08-321-585A-3	Sequence 3, Appl
41	9	75.0	3	1	US-08-446-908-14	Sequence 14, Appl
42	9	75.0	3	1	US-08-231-205A-14	Sequence 14, Appl
43	9	75.0	3	1	US-08-293-150A-22	Sequence 22, Appl
44	9	75.0	3	1	US-08-293-150A-38	Sequence 38, Appl
45	9	75.0	3	3	US-08-447-515-12	Sequence 12, Appl

#### ALIGNMENTS

RESULT 1

US-07-791-213D-23

; Sequence 23, Application US/07791213D

; Patent No. 5409895

; GENERAL INFORMATION:

; APPLICANT: MORISHITA, Hideaki

; APPLICANT: KANAMORI, Toshinori

; APPLICANT: NOBUHARA, Masahiro

; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE

; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME

; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF

; TITLE OF INVENTION: TREATING USING THE SAME

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07791,213D

; FILING DATE: 13-NOV-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 2-306745

; FILING DATE: 13-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,507

; REFERENCE/DOCKET NUMBER: 029650-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-791-213D-23

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 2 C 2

RESULT 2  
US-07-791-213D-39  
; Sequence 39, Application US/07791213D  
; Patent No. 5409895  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791.213D  
; FILING DATE: 13-NOV-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-791-213D-39

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 1 C 1

RESULT 3  
US-08-133-804-9  
; Sequence 9, Application US/08133804  
; Patent No. 5534254  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; TITLE OF INVENTION: Imaging  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/133,804  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kelley, Robin D.  
; REGISTRATION NUMBER: 34,637  
; REFERENCE/DOCKET NUMBER: 2054/22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7477  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..2  
; OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"  
US-08-133-804-9

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 2 C 2

RESULT 4  
US-08-354-240A-12  
; Sequence 12, Application US/08354240A  
; Patent No. 5670356  
; GENERAL INFORMATION:  
; APPLICANT: Sherf, Bruce A.  
; APPLICANT: Wood, Keith V.  
; TITLE OF INVENTION: MODIFIED LUCIFERASE  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dewitt Ross & Stevens, S.C.  
; STREET: 8000 Excelsior Drive, Suite 401  
; CITY: Madison  
; STATE: WI  
; COUNTRY: USA  
; ZIP: 53717-1514  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/354,240A  
; FILING DATE: 12-DEC-1994  
; CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-354-240A-12

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 5
US-08-461-838-9
; Sequence 9, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..2
; OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
; US-08-461-838-9

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 6
US-08-293-150A-23
; Sequence 23, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-150A-23

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 7
US-08-293-150A-39
; Sequence 39, Application US/08293150A
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Patent No. 5792629  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TITLE OF INVENTION: TREATING USING THE SAME  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-293-150A-39

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 1 C 1

RESULT 8  
US-08-461-386-9  
Sequence 9, Application US/08461386  
Patent No. 5837846  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
TITLE OF INVENTION: Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston

STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,386  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..2  
OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"  
US-08-461-386-9

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 2 C 2

RESULT 9  
US-08-465-380-307  
Sequence 307, Application US/08465380  
Patent No. 5863894  
GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,380  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/268  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.  
US-08-465-380-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
Db 1 C 1

RESULT 10  
US-08-486-397-307  
;; Sequence 307, Application US/08486397  
;; Patent No. 5866542  
;; GENERAL INFORMATION:  
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
;; APPLICANT: Peter W. Bergum  
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
;; NUMBER OF SEQUENCES: 357  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; STREET: Suite 4700  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/486,397  
;; FILING DATE: June 5, 1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/269  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.  
US-08-486-397-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
Db 1 C 1

RESULT 11  
US-08-486-399-307  
;; Sequence 307, Application US/08486399  
;; Patent No. 5866543  
;; GENERAL INFORMATION:  
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
;; APPLICANT: Peter W. Bergum  
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
;; NUMBER OF SEQUENCES: 356  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; STREET: Suite 4700  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/486,399  
;; FILING DATE: June 5, 1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/270  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.



US-08-486-399-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 1 C 1

RESULT 12

US-08-461-965-307  
; Sequence 307, Application US/08461965  
; Patent No. 5872098

; GENERAL INFORMATION:

; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
; APPLICANT: Peter W. Bergum

; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
; NUMBER OF SEQUENCES: 356

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,965

; FILING DATE: June 5, 1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/326,110

; FILING DATE: October 18, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BIGGS, SUZANNE L.

; REGISTRATION NUMBER: 30,158

; REFERENCE/DOCKET NUMBER: 210/243

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 307:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; FRAGMENT TYPE: internal fragment

; FEATURE:

; OTHER INFORMATION: Xaa in location 2 is an

; amino acid.

US-08-461-965-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 1 C 1

RESULT 13

US-08-634-641-307

; Sequence 307, Application US/08634641  
; Patent No. 5955294

; GENERAL INFORMATION:

; APPLICANT: Vlasuk, George P. Vlasuk  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Mensens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Gansemans, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew

; APPLICANT: Bergum, Peter W.

; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 356

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/634,641

; FILING DATE: April 19, 1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/13231

; FILING DATE: October 17, 1995

; APPLICATION NUMBER: 08/486,399

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/486,397

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/465,380

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/461,965

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/326,110

; FILING DATE: October 18, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BIGGS, SUZANNE L.

; REGISTRATION NUMBER: 30,158

; REFERENCE/DOCKET NUMBER: 219/136

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 307:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; FRAGMENT TYPE: internal fragment

; FEATURE:

; OTHER INFORMATION: Xaa in location 2 is an

; amino acid.

US-08-634-641-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
Db 1 C 1

## RESULT 14

US-08-818-253-52  
; Sequence 52, Application US/08818253  
; Patent No. 5998204  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Miyawaki, Atsushi  
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
; TITLE OF INVENTION: DETECTION OF ANALYTES  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,253  
; FILING DATE: 14-MAR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Ph.D., Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07257/043001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-818-253-52

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
Db 1 C 1

## RESULT 15

US-09-249-471-307  
; Sequence 307, Application US/09249471  
; Patent No. 6040441  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George Phillip  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Messens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Larocche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Ganssemaus, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew  
; APPLICANT: Berigum, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/249,471  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/809,455  
; FILING DATE: April 17, 1997  
; APPLICATION NUMBER: PCT/US95/13231  
; FILING DATE: October 17, 1995  
; APPLICATION NUMBER: 08/486,399  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/486,397  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/465,380  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/461,965  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 216/270  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; OTHER INFORMATION: amino acid.  
US-09-249-471-307

Query Match 75.0%; Score 9; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
Db 1 C 1

Search completed: February 5, 2001, 12:01:53  
Job time: 335 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 11:57:43 ; Search time 34.92 Seconds  
(without alignments)  
7.778 Million cell updates/sec

Title: US-09-687-267-1  
Perfect score: 12  
Sequence: 1 CXXX 4  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues  
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.66:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	9	75.0	3	A22565	R-phycoerythrin al
2	9	75.0	4	I51049	metallothionein-A
3	9	75.0	4	S43959	Ig mu chain V regi
4	9	75.0	4	S52338	pallidipin - assas
5	9	75.0	5	B22565	R-phycoerythrin al
6	9	75.0	5	F22565	R-phycoerythrin ga
7	9	75.0	5	A33882	cadmium-binding pe
8	9	75.0	5	B45525	actin I - malaria
9	9	75.0	5	S65726	hemoglobin, extrac
10	9	75.0	6	JU0355	lipopeptide WS1279
11	9	75.0	6	C22565	R-phycoerythrin be
12	9	75.0	6	I37027	protamine P1 - gor
13	9	75.0	6	I37263	Y protein - human
14	9	75.0	6	S29881	Na+/K+-exchanging
15	9	75.0	6	H48394	glycoprotein compo
16	9	75.0	6	I67345	MHC H2-K-k cell su
17	9	75.0	6	I65546	MHC H2-L antigen -
18	9	75.0	6	PT0652	T-cell receptor be
19	9	75.0	6	F41946	T-cell receptor ga
20	9	75.0	6	I49421	laminin B1 - weste
21	9	75.0	6	I79564	hypothetical TGL3
22	9	75.0	7	PH1408	Ig heavy chain V r
23	9	75.0	7	A58512	venom heptapeptide
24	9	75.0	7	S08606	hypothetical prote
25	9	75.0	7	S38516	mablinin II chain
26	9	75.0	7	B34818	vicilin 57K chain
27	9	75.0	7	B33882	cadmium-binding he
28	9	75.0	7	A34026	acetylcholinestera
29	9	75.0	7	A12016	formylglycinamide

30	9	75.0	7	2	PH1602	Ig H chain V-D-J r
31	9	75.0	7	2	PH0932	T-cell receptor be
32	9	75.0	7	4	I56695	hypothetical L2 pr
33	9	75.0	8	2	PH1407	Ig heavy chain V r
34	9	75.0	8	2	S59622	metallothionein is
35	9	75.0	8	2	XGHUEU	urine glycopeptide
36	9	75.0	8	2	A25836	L-serine dehydrata
37	9	75.0	8	2	PC1002	leucine--trNA liga
38	9	75.0	8	2	S19288	acylase - Kluyvera
39	9	75.0	8	2	A37521	R-phycoerythrin ga
40	9	75.0	8	2	C61512	variant surface gl
41	9	75.0	8	2	D61512	variant surface gl
42	9	75.0	8	2	PH1618	Ig H chain V-D-J r
43	9	75.0	8	2	PH0803	T-cell receptor al
44	9	75.0	8	2	I57018	gene Cfr protein
45	9	75.0	8	2	PH0934	T-cell receptor be

ALIGNMENTS

RESULT 1  
A22565  
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)  
C:Species: Gastroclonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: A22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601  
A:Accession: A22565  
A:Molecule type: protein  
A:Residues: 1-3 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 1 C 1

RESULT 2  
I51049  
metallothionein-A - rainbow trout (fragment)  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I51049  
R:Olsson, P.E.; Kilin, P.; Erkel, L.J.; Kille, P.  
Eur. J. Biochem. 230, 344-349, 1995  
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)  
A:Reference number: I51049; MUID:95324545  
A:Accession: I51049  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-4 <OLS>  
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 75.0%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 3  
S43959

Ig mu chain V region (clone 13) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
C:Accession: S43959  
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;  
Nucleic Acids Res. 22, 1389-1393, 1994  
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
A:Reference number: S43956; MUID:94248036  
A:Accession: S43959  
A:Molecule type: DNA  
A:Residues: 1-4 <WAG>  
C:Keywords: immunoglobulin

Query Match 75.0%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 2 C 2

RESULT 4  
S5238  
pallidipin - assassin bug (fragment)  
C:Species: Triatoma pallidipennis (assassin bug)  
C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000  
C:Accession: S55238  
R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin  
Biochem. J. 307, 465-470, 1995  
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib  
A:Reference number: S55238; MUID:95251610  
A:Accession: S55238  
A:Molecule type: protein  
A:Residues: 1-4 <HAE>

Query Match 75.0%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 3 C 3

RESULT 5  
B22565  
R-phycoerythrin alpha-2 chain - red alga (Gastrocloonium coulteri) (fragment)  
C:Species: Gastrocloonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: B22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601  
A:Accession: B22565  
A:Molecule type: protein  
A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 2 C 2

RESULT 6  
F22565

R-phycoerythrin gamma-A chain - red alga (Gastrocloonium coulteri) (fragment)  
C:Species: Gastrocloonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: F22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601  
A:Accession: F22565  
A:Molecule type: protein  
A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 3 C 3

RESULT 7  
A33882  
cadmium-binding pentapeptide - downy thornapple  
C:Species: Datura innoxia (downy thornapple)  
C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 18-Jun-1993  
C:Accession: A33882  
R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987

A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plan  
A:Reference number: A94182; MUID:88016144  
A:Accession: A33882  
A:Molecule type: protein  
A:Residues: 1-5 <JAC>

Query Match 75.0%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 2 C 2

RESULT 8  
B45525  
actin I - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C:Date: 03-Jun-1993 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C:Accession: B45525  
R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schrevel  
Mol. Biochem. Parasitol. 35, 167-176, 1989  
A:Title: Stage-specific expression and genomic organization of the actin genes of  
A:Reference number: A45525; MUID:89364996  
A:Accession: B45525  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <WES>  
A:Cross-references: GB:J03988  
A:Note: the authors translated the codon GAA for residue 3 as Gly  
C:Comment: The actin I gene contains no introns.

Query Match 75.0%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 9  
S65726  
hemoglobin, extracellular, chain b - earthworm (lumbricus terrestris) (fragment)  
C:Species: Lumbricus terrestris (common earthworm)  
C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65726  
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.  
Biochim. Biophys. Acta 1292, 273-280, 1996  
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A:Reference number: S65721; MUID:96176855  
A:Accession: S65726  
A>Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <FUS>

Query Match 75.0%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 10  
JU0355  
lipopeptide WS1279 [validated] - Streptomyces willmorei  
C:Species: Streptomyces willmorei  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: JU0355  
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.  
Chem. Pharm. Bull. 39, 607-611, 1991  
A:Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin  
A:Reference number: JU0355; MUID:91300586  
A:Accession: JU0355  
A:Molecule type: protein  
A:Residues: 1-6 <TSU>  
A>Note: the structure was confirmed by synthesis  
C:Keywords: blocked amino end; lipoprotein  
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental  
F:1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 1 C 1

RESULT 11  
C22565  
R-phycoerythrin beta-1 chain - red alga (Gastroleonium coulteri) (fragment)  
C:Species: Gastroleonium coulteri  
C>Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: C22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601  
A:Accession: C22565  
A:Molecule type: protein  
A:Residues: 1-6 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 12  
I37027  
protamine P1 - gorilla (fragment)  
C:Species: Gorilla gorilla (gorilla)  
C>Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jul-2000  
C:Accession: I37027  
R:Queralto, R.; Oliva, R.  
Gene 133, 197-204, 1993  
A:Title: Identification of conserved potential regulatory sequences of the protamine-  
A:Reference number: I37013; MUID:94040810  
A:Accession: I37027  
A>Status: Preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 6 C 6

RESULT 13  
I37263  
Y protein - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I37263  
R:Waechter, G.; Habener, J.F.  
Endocrinology 131, 2010-2015, 1992  
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative  
A:Reference number: I37263; MUID:93010691  
A:Accession: I37263  
A>Status: Preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816  
C:Genetics:  
A:Gene: CREB

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 14  
S29881  
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 07-May-1999  
C:Accession: S29881  
R:Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.  
J. Biol. Chem. 260, 3852-3859, 1985  
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases from  
A:Reference number: S29881; MUID:85131201  
A:Accession: S29881  
A:Molecule type: protein  
A:Residues: 1-6 <WAL>  
A:Experimental source: kidney

C;Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;  
F;4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 2 C 2

## RESULT 15

H48394  
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C;Accession: H48394  
R;Mathur, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
II-like sequences.  
A;Reference number: A48394; MUID:93250576  
A;Accession: H48394  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <MAT>  
A;Experimental source: milk  
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)  
C;Keywords: glycoprotein

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 6 C 6

Search completed: February 5, 2001, 12:02:32  
Job time: 289 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:23 ; Search time 20.72 Seconds  
(without alignments)  
6.234 Million cell updates/sec

Title: US-09-687-267-1

Perfect score: 12

Sequence: 1 CXXX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	9	75.0	8 1 ACT_CARMA	P80709 carcinus ma
2	9	75.0	8 1 GLUR_HUMAN	P02729 homo sapien
3	9	75.0	9 1 CCAP_CARMA	P38556 carcinus ma
4	9	75.0	9 1 CONO_CONGE	P05486 conus geogr
5	9	75.0	9 1 CONO_CONST	P05487 conus stria
6	9	75.0	9 1 DNEFL_LOCM1	P16339 locusta mig
7	9	75.0	9 1 ISOT_CYPCA	P42993 cyprinus ca
8	9	75.0	9 1 MGMT_BOVIN	P29177 bos taurus
9	9	75.0	9 1 OXYA_SCYCA	P42996 scyllorhinu
10	9	75.0	9 1 OXYA_SQUAC	P42997 squalus aca
11	9	75.0	9 1 OXYF_SCYCA	P42997 scyllorhinu
12	9	75.0	9 1 OXYT_BUFRE	P42995 bufo regula
13	9	75.0	9 1 OXYT_CYPCA	P23879 cyprinus ca
14	9	75.0	9 1 OXYT_EISFO	P42998 eisenia foe
15	9	75.0	9 1 OXYT_OCTUV	P80027 octopus vul
16	9	75.0	9 1 OXYT_RABIT	P32878 oryctolagus
17	9	75.0	9 1 OXYT_RAJCL	P42994 raja clavav
18	9	75.0	9 1 OXYT_SQUAC	P43000 squalus aca
19	9	75.0	9 1 RS11_SALTY	O54296 salmonella
20	9	75.0	9 1 SAP_STOVA	P24047 stomopneute
21	9	75.0	9 1 TAL1_PICUA	P17440 pichia jadi
22	9	75.0	9 1 TAL3_PICUA	P17441 pichia jadi
23	9	75.0	10 1 GLEM_HUMAN	P02728 homo sapien
24	9	75.0	10 1 GON2_CHEPR	P80678 chelyosoma
25	9	75.0	10 1 RCA_PINPS	P81084 pinus pinas
26	9	75.0	12 1 CXAL_CONIM	P50983 conus imper
27	9	75.0	12 1 N040_IOTJA	O22426 lotus japon
28	9	75.0	12 1 N040_SESRO	O24369 sesbania ro
29	9	75.0	12 1 N040_SOYBN	P55960 glycine max
30	9	75.0	12 1 RR16_GINBI	P36207 ginkgo bilo
31	9	75.0	12 1 TAL1_TREME	P01371 tremella me
32	9	75.0	12 1 UR2A_CATCO	P04558 catostomus
33	9	75.0	12 1 UR2B_CATCO	P04559 catostomus

34 9 75.0 12 1 UR2B\_CYPCA P04561 cyprinus ca  
35 9 75.0 12 1 UR2\_GILMI P01147 gillichyus  
36 9 75.0 12 1 UR2\_POLSP P81022 polyodon sp  
37 9 75.0 12 1 UR2\_SCYCA P35490 scyllorhinu  
38 9 75.0 12 1 YZPV\_ECOLI P17776 escherichia  
39 9 75.0 13 1 ACT7\_SOYBN P15987 glycine max  
40 9 75.0 13 1 CXAL\_CONST P15471 conus stria  
41 9 75.0 13 1 CXA2\_CONGE P01520 conus geogr  
42 9 75.0 13 1 CXAA\_CONST P28878 conus stria  
43 9 75.0 13 1 CXET\_CONTE P81755 conus texti  
44 9 75.0 13 1 GER1\_HORVU P28525 hordeum vul  
45 9 75.0 13 1 GER2\_HORVU P28526 hordeum vul

#### ALIGNMENTS

RESULT 1  
ACT\_CARMA STANDARD; PRT; 8 AA.  
ID ACT\_CARMA  
AC P80709;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ACTIN (FRAGMENT).  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
RN [1]  
RP SEQUENCE.  
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
RA Baghdassarian D.;  
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";  
RL Endocrine 5:23-32(1996).  
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED  
IN ALL EUKARYOTIC CELLS.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
6.8, ITS MW IS: 46 KDA.  
CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.  
DR INTERPRO: IPR000279; .  
DR PROSITE: PS00406; ACTINS\_1; PARTIAL.  
DR PROSITE: PS00432; ACTINS\_2; PARTIAL.  
DR PROSITE: PS01132; ACTINS\_ACT\_LIKE; PARTIAL.  
KW Structural protein.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
Db 2 C 2

RESULT 2  
GLUR\_HUMAN STANDARD; PRT; 8 AA.  
ID GLUR\_HUMAN  
AC P02729;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE URINE GLYCOPETIDE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]



RP SEQUENCE.  
RX MEDLINE=72062338; PubMed=5126885;  
RA Lote C.J., Weiss J.B.;  
RT "Identification in urine of a low-molecular-weight highly polar  
RT glycopeptide containing cysteinyl-galactose.";  
RL Biochem. J. 123:25P-25P(1971).  
CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE  
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN  
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A  
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.  
DR PIR: A03188; XGHUEU.  
KW Glycoprotein.  
FT CARBOHYD 1 1 S-LINKED (GAL. .).  
SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5B1EB1E CRC64;  
  
Query Match 75.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 C 1  
DB 1 C 1  
  
RESULT 3  
CCAP\_CARMA STANDARD; PRT; 9 AA.  
ID CCAP\_CARMA STANDARD; PRT; 9 AA.  
AC P38556;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CARDIOACTIVE PEPTIDE (CCAP).  
OS Carcinus maenas (Common shore crab) (Green crab),  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),  
OS Tenebrio molitor (Yellow mealworm), and  
OS Spodoptera eridania (Southern armyworm).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C.MAENAS; TISSUE=PERICARDIAL ORGANS;  
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;  
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
RT shore crab Carcinus maenas";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).  
RN [2]  
RP SEQUENCE.  
RX MEDLINE=93050243; PubMed=1426284;  
RA Cheung C.C., Loi P.K., Sylvester A.W., Lee T.D., Tublitz N.J.;  
RT "Primary structure of a cardioactive neuropeptide from the tobacco  
RT hawkmoth, Manduca sexta.";  
RL FEBS Lett. 313:165-168(1992).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=T.MOLITOR, AND S.ERIDANIA; TISSUE=HEAD;  
RX MEDLINE=94176032; PubMed=8129851;  
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,  
RA Schooley D.A.;  
RT "Isolation and identification of a cardioactive peptide from Tenebrio  
RT molitor and Spodoptera eridania.";  
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).  
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.  
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
CC INTO THE HEMOLYPH.  
DR PIR: A26363; A26363.  
DR PIR: S27233; S27233.  
KW Neuropeptide; Amidation.  
FT DISULFID 3 9  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 C 1  
DB 3 C 3  
  
RESULT 4  
CONO\_CONGE STANDARD; PRT; 9 AA.  
ID CONO\_CONGE STANDARD; PRT; 9 AA.  
AC P05486;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE LYS-CONOPRESSIN G.  
OS Conus geographus (Geography cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88058932; PubMed=3680228;  
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
RA Gray W.R., Olivera B.M.;  
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of  
RT peptides from Conus geographus and Conus straitus venoms.";  
RL J. Biol. Chem. 262:15821-15824(1987).  
RN [2]  
RP REVIEW.  
RX MEDLINE=89024586; PubMed=3052286;  
RA Gray W.R., Olivera B.M., Cruz L.J.;  
RT "Peptide toxins from venomous Conus snails.";  
RL Annu. Rev. Biochem. 57:665-700(1988).  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR: A28495; A28495.  
DR INTERPRO: IPR000981;  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;  
  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 C 1  
DB 1 C 1  
  
RESULT 5  
CONO\_CONST STANDARD; PRT; 9 AA.  
ID CONO\_CONST STANDARD; PRT; 9 AA.  
AC P05487;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ARG-CONOPRESSIN S.  
OS Conus striatus (Striated cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88058932; PubMed=3680228;  
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
RA Gray W.R., Olivera B.M.;  
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of

RT peptides from Conus geographus and Conus straitus venoms.";  
RL J. Biol. Chem. 262:15821-15824(1987).  
RN [2]

RP REVIEW.  
RX MEDLINE=89024586; PubMed=3052286;  
RA Gray W.R., Olivera B.M., Cruz L.J.;  
RT "Peptide toxins from venomous Conus snails.";  
RL Annu. Rev. Biochem. 57:665-700(1988).  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR: B28495; B28495.  
DR INTERPRO: IPR000981; -.  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 1 C 1

RESULT 6

DNFL\_LOCMI STANDARD; PRT; 9 AA.  
AC P16339;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE LOCUPRESSIN (DIURETIC NEUROPEPTIDE F1/F2).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
OC pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;  
OC Acridomorpha; Acridoidea; Acrididae; Locusta.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=SUBESOPHAGEAL GANGLION, AND THORACIC GANGLION;  
RX MEDLINE=88077077; PubMed=3689410;  
RA Proulx J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,  
RA Delaage M., Schooley D.A.;  
RT "Identification of an arginine vasopressin-like diuretic hormone from  
RT Locusta migratoria.";  
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).  
CC -!- FUNCTION: DIURETIC HORMONE.  
CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR: A29477; A29477.  
DR INTERPRO: IPR000981; -.  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Neuropeptide; Amidation.  
FT DISULFID 1 6  
FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).  
FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 1 C 1

RESULT 7

ISOT\_CYPCA STANDARD; PRT; 9 AA.  
ID ISOT\_CYPCA  
AC P42993;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ISOTOCIN.  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=PIUITARY;  
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
RT "Characterization of neurohypophyseal hormones from a fresh water bony  
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea  
RT water bony fishns.";  
RL Comp. Biochem. Physiol. 14:245-254(1965).  
CC -!- FUNCTION: ANTI-DIURETIC HORMONE.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR: A61364; A61364.  
DR INTERPRO: IPR000981; -.  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 1 C 1

RESULT 8

MGMT\_BOVIN STANDARD; PRT; 9 AA.  
ID MGMT\_BOVIN  
AC P29177;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-  
DE METHYLGUANINE-DNA METHYLTRANSFERASE) (FRAGMENT).  
GN MGMT.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=THYMUS;  
RX MEDLINE=90174912; PubMed=2308822;  
RA Rydberg B., Hall J., Karren P.;  
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA  
RT methyltransferase.";  
RL Nucleic Acids Res. 18:17-21(1990).  
CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY  
CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE  
CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS  
CC IRREVERSIBLY INACTIVATED.  
CC -!- CATALYTIC ACTIVITY: DNA (CONTAINING O6-METHYLGUANINE) + PROTEIN  
CC L-CYSTEINE -> DNA (WITHOUT O6-METHYLGUANINE) + PROTEIN S-METHYL-  
CC L-CYSTEINE.  
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE  
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.  
DR INTERPRO: IPR001497; .

DR PROSITE; PS00374; MGMT; PARTIAL.  
KW DNA repair; Transferase; Methyltransferase.  
FT NON\_TER 1  
FT ACT\_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 9 C 9

RESULT 9  
OXYA\_SCYCA STANDARD; PRT; 9 AA.  
AC P42996;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ASPARTOCIN.  
OS Scyllorhinus canicula (Spotted dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
OC Scyllorhinidae; Scyllorhinus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=PITUITARY;  
RX MEDLINE=95062247; PubMed=7972045;  
RA Chauvet J., Rouille Y., Chauvet M.-T., Acher R.;  
RT "Special evolution of neurohypophyseal hormones in cartilaginous fishes: aspartocin and phasvatocin, two oxytocin-like peptides isolated from the spotted dogfish (Scyllorhinus caniculus).";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).  
CC 1- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.  
CC 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.  
DR INTERPRO: IPR000981; -.  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 1 C 1

RESULT 10  
OXYA\_SQUAC STANDARD; PRT; 9 AA.  
AC P42999;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ASPARTOCIN (ASPARTOCIN).  
OS Squalus acanthias (Spiny dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squala; Squaloidi; Squalidae; Squalus.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=73031172; PubMed=5083097;  
RA Acher R., Chauvet J., Chauvet M.-T.;

RT "Phylogeny of the neurohypophyseal hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";  
RL Eur. J. Biochem. 29:12-19(1972).  
RN [2]  
RP SEQUENCE.  
RX MEDLINE=72128038; PubMed=4622083;  
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;  
RT "Identification of 2 new neurohypophyseal hormones, vallitocin (Val18-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the RT spiny dog-fish (Squalus acanthias).";  
RT C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).  
CC 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.  
DR INTERPRO: IPR000981; -.  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 1 C 1

RESULT 11  
OXYF\_SCYCA STANDARD; PRT; 9 AA.  
AC P42997;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE PHASVATOCIN.  
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
OC Scyllorhinidae; Scyllorhinus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=PITUITARY;  
RX MEDLINE=95062247; PubMed=7972045;  
RA Chauvet J., Rouille Y., Chauvet M.-T., Acher R.;  
RT "Special evolution of neurohypophyseal hormones in cartilaginous fishes: asvatocin and phasvatocin, two oxytocin-like peptides isolated from the spotted dogfish (Scyllorhinus caniculus).";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).  
CC 1- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.  
CC 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.  
DR INTERPRO: IPR000981; -.  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 1 C 1

RESULT 12  
OXYT\_BUFRE

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ID OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE SERITOCIN.
OS Bufo regularis (African toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufonidae;
OC Bufo.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY NEUROINTERMEDIATE LOBE;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIN ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981;
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT MOD_RES 9 6
FT DISULFID 1 1
FT SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 13
OXYT_CYPCA STANDARD; PRT; 9 AA.
ID OXYT_CYPCA
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE VASOTOCIN.
OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
RN [1]
RP SEQUENCE.
RC SPECIES=C. CARPIO; TISSUE=PITUITARY;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishs.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P. MARINUS; TISSUE=PITUITARY;
RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawauchi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: B61364; B61364.
DR PIR: S06375; S06375.
DR INTERPRO: IPR000981;
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Amidation.
FT MOD_RES 9 6
FT DISULFID 1 1
FT SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 15
OXYT_OCTVU STANDARD; PRT; 9 AA.
ID OXYT_OCTVU
AC P80027;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CEPHALOTOCIN.
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
RN [1]
RP SEQUENCE.
RC TISSUE=NERVE ENDINGS;

```

RX MEDLINE-92270139; PubMed-1589145;  
RA Reich G.;  
RT "A new peptide of the oxytocin/vasopressin family isolated from  
RT nerves of the cephalopod Octopus vulgaris.";  
RL Neurosci. Lett. 134:191-194(1992).  
CC -!- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA  
CC CAVA.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR INTERPRO; IPR000981; -.  
DR PFAM; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1072 MW; 17FF476EB45409DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 C 1  
Db 1 C 1

Search completed: February 5, 2001, 12:06:02  
Job time: 279 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:00:49 ; Search time 57.72 Seconds  
(without alignments)  
8.123 Million cell updates/sec

Title: US-09-687-267-1

Perfect score: 12

Sequence: 1 CXXX 4

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_15:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	75.0	6	Q08720	Q08720 homo sapien
2	9	75.0	7	P70804	P70804 azotobacter
3	9	75.0	7	O55184	O55184 rattus norv
4	9	75.0	7	Q66113	Q66113 cherry leaf
5	9	75.0	7	Q67113	Q67113 influenza a
6	9	75.0	7	Q9YVE3	Q9YVE3 human adeno
7	9	75.0	7	Q9YI90	Q9YI90 human adeno
8	9	75.0	7	Q9YI09	Q9YI09 human adeno
9	9	75.0	7	Q42564	Q42564 fugu rubrip
10	9	75.0	8	O32560	O32560 escherichia
11	9	75.0	8	Q15888	Q15888 homo sapien
12	9	75.0	8	Q15890	Q15890 homo sapien
13	9	75.0	8	Q15900	Q15900 homo sapien
14	9	75.0	8	Q9Y4X6	Q9Y4X6 homo sapien
15	9	75.0	8	O02831	O02831 oryctolagus
16	9	75.0	8	Q9TRY3	Q9TRY3 sus sp. ins
17	9	75.0	8	Q9SAY7	Q9SAY7 dioscorea t
18	9	75.0	8	Q11P70243	P70243 mus musculu
19	9	75.0	8	Q11Q35835	O35835 rattus norv

20	9	75.0	8	12	Q85562	Q85562 moloney mur
21	9	75.0	8	13	Q90493	Q90493 eopsaltria
22	9	75.0	8	13	Q90498	Q90498 erythrura g
23	9	75.0	8	13	Q91098	Q91098 manorina me
24	9	75.0	9	2	Q47063	Q47063 escherichia
25	9	75.0	9	4	Q15999	Q15999 homo sapien
26	9	75.0	9	4	Q99887	Q99887 homo sapien
27	9	75.0	9	6	Q9XI05	Q9XI05 macropus ru
28	9	75.0	9	6	Q9TUY0	Q9TUY0 monodelphis
29	9	75.0	9	9	Q38340	Q38340 lactococcus
30	9	75.0	9	11	Q9QZ88	Q9QZ88 mus musculu
31	9	75.0	9	11	P97889	P97889 rattus norv
32	9	75.0	9	12	Q69473	Q69473 human herpe
33	9	75.0	9	12	O12096	O12096 caprine art
34	9	75.0	9	12	O12098	O12098 caprine art
35	9	75.0	9	12	O12100	O12100 caprine art
36	9	75.0	9	12	O12102	O12102 caprine art
37	9	75.0	9	12	O12104	O12104 caprine art
38	9	75.0	9	12	O90350	O90350 heparitis g
39	9	75.0	10	2	O50032	O50032 mycobacteri
40	9	75.0	10	2	Q47475	Q47475 escherichia
41	9	75.0	10	2	Q48469	Q48469 klebsiella
42	9	75.0	10	2	O9K343	O9K343 escherichia
43	9	75.0	10	3	Q9UW22	Q9UW22 schizophyll
44	9	75.0	10	4	Q13318	Q13318 homo sapien
45	9	75.0	10	4	Q9UN90	Q9UN90 homo sapien

#### ALIGNMENTS

RESULT 1

Q08720 ID Q08720 PRELIMINARY; PRT; 6 AA.  
AC Q08720; DT 01-NOV-1996 (TREMREL. 01, Created)  
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)  
DE Y PROTEIN (FRAGMENT).  
GN CREB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93010691; PubMed=1396344;  
RA Waeber G., Habener J.F.;  
RT "Novel testis germ cell-specific transcript of the CREB gene contains  
RT an alternatively spliced exon with multiple in-frame stop codons.";  
RL Endocrinology 131:2010-2015(1992).  
DR EMBL; X68994; CAA48780.1; -;  
FT NON\_TER 1  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

DB 4 C 4

RESULT 2

P70804 ID P70804 PRELIMINARY; PRT; 7 AA.  
AC P70804;  
DT 01-FEB-1997 (TREMREL. 02, Created)  
DT 01-FEB-1997 (TREMREL. 02, Last sequence update)  
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)

DE ALGG GENE (FRAGMENT).

GN ALGT.  
OS Azotobacter vinelandii.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Azotobacter.  
OX NCBI\_TaxID=354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E;  
RX MEDLINE=96427318; PubMed=8830682;  
RA Rehm B.H.A., Ertesvag H., Valla S.;  
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is  
RT part of an alg gene cluster physically organized in a manner similar  
RT to that in Pseudomonas aeruginosa.";  
RL J. Bacteriol. 178:5884-5889(1996).  
DR EMBL; X87973; CAA61230.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 1 C 1

RESULT 3

O55184 PRELIMINARY; PRT; 7 AA.

AC O55184;  
DT 01-JUN-1998 (TRENBLrel. 06, Created)  
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
DE ORPHAN RECEPTOR TR4-NS (FRAGMENT).  
GN TR4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96198747; PubMed=8612486;  
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,  
RA Detera-Wadleigh S.D.;  
RT "Splice variants of rat TR4 orphan receptor: differential expression  
RT of novel sequences in the 5'-untranslated region and C-terminal  
RT domain.";  
RL Endocrinology 137:1562-1571(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96299786; PubMed=8661150;  
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;  
RT "New variants of the human and rat nuclear hormone receptor, TR4:  
RT expression and chromosomal localization of the human gene.";  
RL Genomics 35:361-366(1996).  
DR EMBL; U59454; AAB91433.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 75.0%; Score 9; DB 11; Length 7;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 3 C 3

RESULT 4

O66113 PRELIMINARY; PRT; 7 AA.

AC O66113;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
DE C-TERMINUS OF THE VIRAL REPLICASE (FRAGMENT).  
OS Cherry leaf roll virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;  
OC Nepovirus.  
OX NCBI\_TaxID=12615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WALNUT;  
RA Borja M.;  
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INTA.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WALNUT;  
RX MEDLINE=96124520; PubMed=8560786;  
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;  
RT "Long, nearly identical untranslated sequences at the 3' terminal  
RT regions of the genomic RNAs of cherry leafroll virus (walnut  
RT strain)";  
RL Virus Genes 10:245-252(1995).  
DR EMBL; Z34265; CAA84019.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 5

O67113 PRELIMINARY; PRT; 7 AA.

AC O67113;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
DE (UDORN/72) HEMAGGLUTININ (SEG 4) CDNA, 3' END (FRAGMENT).  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81001892; PubMed=7407922;  
RA Dhar R., Chanock R.M., Lai C.J.;  
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza  
RT viral mRNA deduced from cloned complete genomic sequences.";  
RL Cell 21:495-500(1980).  
DR EMBL; M25045; AAA43202.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 3 C 3

```
RESULT 6
Q9YVE3 ID Q9YVE3 PRELIMINARY; PRT; 7 AA.
AC Q9YVE3;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GOMEN;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
RT acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065065; AAD03662.1; -.
DR EMBL; AF065065; AAD03662.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 6 C 6

RESULT 7
Q9YI0 ID Q9YI0 PRELIMINARY; PRT; 7 AA.
AC Q9YI0;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7a.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=85755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KN T96-0620, S-1058, CL 68578;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
RT acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065068; AAD03668.1; -.
DR EMBL; AF065065; AAD03664.1; -.
DR EMBL; AF065067; AAD03666.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 6 C 6

RESULT 8
Q9YI09 ID Q9YI09 PRELIMINARY; PRT; 7 AA.
AC Q9YI09;
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DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 4.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2-G 95-873, RI-67, 55142;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
RT acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03659.1; -.
DR EMBL; AF065062; AAD03653.1; -.
DR EMBL; AF065063; AAD03656.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 6 C 6

RESULT 9
O42564 ID O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT (FRAGMENT).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
DR EMBL; U97673; AAB80916.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 75.0%; Score 9; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 5 C 5

RESULT 10
O32560 ID O32560 PRELIMINARY; PRT; 8 AA.
AC O32560;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
```



DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DE 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
DE PROIONATE KINASE (FRAGMENT).  
GN TDCD.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-W3110;  
RA Hesslinger C., Savers G.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ001620; CAA04875.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 6 C 6  
RESULT 11  
Q15888 PRELIMINARY; PRT; 8 AA.  
AC Q15888;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
DE (CLONE XP15H8A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32059; AAA73878.1; -.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 5 C 5  
RESULT 12  
Q15890 PRELIMINARY; PRT; 8 AA.  
AC Q15890;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)

DE (CLONE XP19C12A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32083; AAA73880.1; -.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 4 C 4

RESULT 13  
Q15900 PRELIMINARY; PRT; 8 AA.  
AC Q15900;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
DE (CLONE XP7B11A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32079; AAA73890.1; -.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAEB1 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 2 C 2  
RESULT 14  
Q9Y4X6 PRELIMINARY; PRT; 8 AA.  
AC Q9Y4X6;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE NUCLEAR LIM INTERACTOR (FRAGMENT).  
GN NLI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

```
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
RA Schroth A., Boden J., Royer-Pokora B.;
RT "Genomic structure, alternative transcripts and chromosomal
RT localization of the human LIM domain binding protein 1 gene
RT LDB1/NLI.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ243097; CAB45408.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 767 MW; EE6EBDD8B862D5B6 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 5 C 5

RESULT 15
O02831 PRELIMINARY; PRT; 8 AA.
AC O02831;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCB1_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9637739; PubMed=8783186;
RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 75.0%; Score 9; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 4 C 4
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Search completed: February 5, 2001, 12:05:38  
Job time: 289 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:19 ; Search time 42.35 Seconds  
(without alignments)  
3.230 Million cell updates/sec

Title: US-09-687-267-4

Perfect score: 12

Sequence: 1 KCXX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_36.\*

- 1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.\*
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- 10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	3	P10301	Sequence which cor
2	9	75.0	3	P90982	Binding receptor w
3	9	75.0	3	P91660	Synthetic peptide
4	9	75.0	3	R34022	Metal trapping pep
5	9	75.0	3	R34023	Metal trapping pep
6	9	75.0	3	R51439	IGF-1 analogue N-t
7	9	75.0	3	R51440	IGF-1 analogue N-t
8	9	75.0	3	R51441	IGF-1 analogue N-t
9	9	75.0	3	W19847	Human interleukin-
10	9	75.0	3	W56231	Anti-inflammatory
11	9	75.0	3	W56211	Anti-inflammatory
12	9	75.0	3	W56200	Anti-inflammatory

13	9	75.0	3	19	W56172	Anti-inflammatory
14	9	75.0	3	20	W88037	Peptide used in th
15	9	75.0	3	21	Y51896	Biostatin TR232 sy
16	9	75.0	4	2	P10138	Sequence of antiin
17	9	75.0	4	2	P10093	Sequence of peptid
18	9	75.0	4	2	P10382	Enkephalin-like an
19	9	75.0	4	3	P20217	Analgesic and neur
20	9	75.0	4	4	P30083	Sequence of chromo
21	9	75.0	4	4	P30085	Sequence of chromo
22	9	75.0	4	5	P40538	Sequence of cyclic
23	9	75.0	4	5	P40539	Sequence of cyclic
24	9	75.0	4	8	P70833	Sequence encoded b
25	9	75.0	4	10	P91661	Synthetic peptide
26	9	75.0	4	12	R11077	Peptide fragment #
27	9	75.0	4	12	R11079	Peptide fragment #
28	9	75.0	4	12	R11508	Thioredoxin active
29	9	75.0	4	12	R11744	Cyclic platelet ag
30	9	75.0	4	12	R11745	Cyclic platelet ag
31	9	75.0	4	12	R12554	Ocular pressure re
32	9	75.0	4	12	R13935	Antibiotic FK9017
33	9	75.0	4	12	R14723	Farnesyl-protein t
34	9	75.0	4	12	R15751	Farnesyl-protein t
35	9	75.0	4	12	R15752	Farnesyl-protein t
36	9	75.0	4	12	R15753	Farnesyl-protein t
37	9	75.0	4	12	R15754	Farnesyl-protein t
38	9	75.0	4	12	R15755	Farnesyl-protein t
39	9	75.0	4	12	R15756	Farnesyl-protein t
40	9	75.0	4	12	R15757	Farnesyl-protein t
41	9	75.0	4	12	R15758	Farnesyl-protein t
42	9	75.0	4	12	R15759	Farnesyl-protein t
43	9	75.0	4	12	R15760	Farnesyl-protein t
44	9	75.0	4	12	R15761	Farnesyl-protein t
45	9	75.0	4	21	Y80840	Fluorophore-label

ALIGNMENTS

RESULT 1	
P10301	
ID P10301 standard; Protein; 3 AA.	
XX	
AC P10301;	
XX	
DT 19-AUG-1992 (first entry)	
XX	
DE Sequence which corresp. to residues 19-21 of insulin A chain.	
XX	
KW Cystine peptide; insulin activity; hormone; diabetes therapy;	
KW antidiabetic agent.	
XX	
OS Mammal.	
XX	
FH Key	Location/Qualifiers
FT Disulfide-bond 2	
FT	/note= "bonded to Cys(5) of P10115, which is
FT	residue 19 of the B chain fragment
FT	B15-27"
XX	
PN DD147942-A.	
XX	
PD 29-APR-1981.	
XX	
PF 01-FEB-1980; 90DD-0011868.	
XX	
PR 20-AUG-1979; 79DD-0215100.	
XX	
PA (LOSS/) LOSSE G.	
XX	
PI Losse G, Stange H;	
XX	
DR WPI; 1981-53498D/30 (53498D).	
XX	

PT Cysteine peptide(s) with antidiabetic activity - contg. fragments  
XX of insulin A and B chains

PS Claim 1; Page 10; lipp; German.

XX The inventors claim the prepn. of new cysteine peptides with insulin-  
CC like activity. The new peptides comprise a sequence with corresp. to  
CC a central portion of the insulin B chain (esp. B15-27) and a  
CC cysteine-contg. peptide with an AA sequence corresp. to a terminal  
CC portion of the insulin A chain (esp. A1-7). The new cysteine  
CC peptides are antidiabetic agents with appreciable insulin activity  
CC (lower than that of insulin itself) and low antigenic activity.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 2; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

DB 2 C 2

RESULT 2

P90982  
ID P90982 standard; peptide; 3 AA.

AC P90982;

XX 06-JUN-1990 (first entry)

XX Binding receptor with selectivity for a target ligand, borne by  
DE an article for inactivating toxic materials.

XX Toxic material; inactivator; organophosphorous cpds.; nerve poison;  
KW pesticide; decontaminant; military.

XX WO8902920-A.

XX 06-APR-1989.

XX 04-OCT-1988; 88WO-US03422.

XX 05-OCT-1987; 87US-0105312.

XX (LITT ) LITTLE AD INC.

PA Taylor RF;

XX WPI; 1989-114395/15.

XX Article for inactivating toxic materials, eg organo-phosphorous cpds. -  
PT comprises solid carrier bearing target ligand binding receptor  
PT and ligand-degrading receptor, pref. enzyme

XX Claim 7a; page 42; 57pp; English.

XX The article for inactivating a toxic material comprises a solid carrier  
CC bearing a first receptor which binds the target ligand and a second  
CC receptor which degrades the target ligand. This synthetic peptide is  
CC a preferred first receptor. The article may be used for covering  
CC surfaces to protect or decontaminate the surface. The article is esp. for  
CC degrading toxic organic cpds., esp. organophosphorous cpds., (eg  
CC pesticides and nerve poisons, bacteria and viruses, in environmental,  
CC chemical, military and industrial settings.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

DB 2 C 2

RESULT 3

P91660

ID P91660 standard; protein; 3 AA.

XX AC P91660;

XX 29-JUN-1990 (first entry)

XX Synthetic peptide corresp. to residues 12-14 of naturally occurring  
DE epidermal growth factor (EGF).

XX Epidermal growth factor; angiogenesis; synthetic peptide.

XX Key

FT Misc-difference 1

FT /label=OTHER

FT /note="H-Gly"

FT Misc-difference 3

FT /label=OTHER

FT /note="(aceto amido methyl) NH2-Cys"

XX WO8901489-A.

XX 23-FEB-1989.

XX 10-AUG-1988; 88WO-AU00300.

XX 10-AUG-1987; 87AU-0003629.

XX (CSIR ) COMMONWEALTH SCIENT ORG.

XX McAuslan BR;

XX WPI; 1989-068852/09.

XX Synthetic peptide active in stimulating angiogenesis -  
PT has sequences corresponding to amino acid sequences occurring in  
PT epidermal growth factor.

XX Claim 3; page 10; lipp; English.

XX The inventors claim synthetic peptides which correspond to sequences  
CC occurring in EGF, but excluding EGF. The peptides are angiogenic  
CC and have corresp. applications, eg for the healing of wounds and  
CC burns. Their relative shortness means that they pose fewer synthesis  
CC problems than the entire EGF molecule. They can be admin. singly or  
CC association with each other or in association with an angiogenic  
CC stimulator.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

DB 3 C 3

RESULT 4

R34022

ID R34022 standard; peptide; 3 AA.

XX AC R34022;

XX 19-MAY-1993 (first entry)  
 DT Metal trapping peptide intermediate.  
 DE Electrostatic interaction; metalloprotein; binding site;  
 XX protecting group.  
 KW Synthetic.  
 XX  
 OS Key Location/Qualifiers  
 FH Modified-site 1 /note= "Boc protected"  
 FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH  
 FT of cysteine"  
 FT Modified-site 3 /note= "OME protected"  
 FT  
 FT JP04346999-A.  
 PN 02-DEC-1992.  
 PD 24-MAY-1991; 91JP-0120196.  
 XX 24-MAY-1991; 91JP-0120196.  
 XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.  
 PA WPI; 1993-021449/03.  
 DR New acyclic peptide with metal trapping activity - exhibits in  
 XX vivo metal transporting action and can be used as drug,  
 PT diagnostic agent or functional material  
 PT Claim 3; Page 2; 9pp; Japanese.  
 PS The acyclic peptide (see R31340) with metal trapping activity may be  
 XX produced by fragment condensation using the peptide fragments given in  
 CC R34022-29.  
 CC Sequence 3 AA;  
 XX  
 XX Query Match 75.0%; Score 9; DB 14; Length 3;  
 DT Best Local Similarity 100.0%; Pred. No. 0;  
 DE Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 2 C 2  
 DB 2 C 2  
 XX  
 XX RESULT 5  
 ID R34023 standard; peptide; 3 AA.  
 XX  
 AC R34023;  
 XX  
 DT 19-MAY-1993 (first entry)  
 XX  
 DE Metal trapping peptide intermediate.  
 XX  
 KW Electrostatic interaction; metalloprotein; binding site;  
 KW protecting group.  
 XX  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "HCl.H-Val"  
 FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH  
 FT

FT Modified-site 3 of cysteine"  
 FT /note= "OME protected"  
 XX  
 PN JP04346999-A.  
 XX  
 PD 02-DEC-1992.  
 XX  
 PF 24-MAY-1991; 91JP-0120196.  
 XX  
 PR 24-MAY-1991; 91JP-0120196.  
 XX  
 PA (ICHI-) ICHIKAWA GOSEI KAGAKU KK.  
 XX  
 DR WPI; 1993-021449/03.  
 XX  
 PT New acyclic peptide with metal trapping activity - exhibits in  
 PT vivo metal transporting action and can be used as drug,  
 PT diagnostic agent or functional material  
 XX  
 PS Claim 3; Page 2; 9pp; Japanese.  
 XX  
 CC The acyclic peptide (see R31340) with metal trapping activity may be  
 CC produced by fragment condensation using the peptide fragments given in  
 CC R34022-29.  
 XX  
 XX Sequence 3 AA;  
 XX  
 XX Query Match 75.0%; Score 9; DB 14; Length 3;  
 DT Best Local Similarity 100.0%; Pred. No. 0;  
 DE Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 2 C 2  
 DB 2 C 2  
 XX  
 XX RESULT 6  
 ID R51439 standard; peptide; 3 AA.  
 XX  
 AC R51439;  
 XX  
 DT 27-OCT-1994 (first entry)  
 XX  
 DE IGF-1 analogue N-terminal.  
 XX  
 KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;  
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9406445-A.  
 XX  
 PD 31-MAR-1994.  
 XX  
 PF 02-SEP-1993; 93WO-US08279.  
 XX  
 PR 17-SEP-1992; 92US-0947035.  
 XX  
 PA (EMBR-) EMBREX INC.  
 PA (GROP-) GROPEP PTY LTD.  
 PA (USDA ) US SEC OF AGRIC.  
 XX  
 PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;  
 PI Walton PE;  
 XX  
 DR WPI; 1994-118144/14.  
 XX  
 PT Increasing growth of birds - with insulin-like growth factor  
 PT delivered to the egg before hatching esp. for increasing wt. gain  
 PT in chickens.  
 PT

XX PS Claim 6; Page 37; 45pp; English.

XX CC Growth of birds is increased by (a) admin. to the bird, in ovo,

XX CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;

XX CC (b) incubating to hatch and (c) growing the birds for at least 3

XX CC weeks after hatch.

XX CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or

XX CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,

XX CC partic. Gly and the Thr normally adjacent to Glu can be replaced

XX CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal

XX CC given in R51439-49.

XX CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced

XX CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent

XX CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.

XX CC comprises the N-terminal given in R51450-53.

XX CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human

XX CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid

XX CC N-terminal extension.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 15; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

DB 3 C 3

RESULT 7

R51440

ID R51440 standard; peptide; 3 AA.

XX AC R51440;

XX DT 27-OCT-1994 (first entry)

XX DE IGF-1 analogue N-terminal.

XX KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;

XX KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.

XX OS Homo sapiens.

XX PN WO9406445-A.

XX PD 31-MAR-1994.

XX PF 02-SEP-1993; 93WO-US08279.

XX PR 17-SEP-1992; 92US-0947035.

XX PA (EMBR-) EMBREX INC.

XX PA (GROP-) GROPEP PTY LTD.

XX PA (USDA) US SEC OF AGRIC.

XX PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;

XX PI Walton PE;

XX WPI; 1994-118144/14.

XX PT Increasing growth of birds - with insulin-like growth factor

XX PT delivered to the egg before hatching esp. for increasing wt. gain

XX PT in chickens.

XX PS Claim 6; Page 37; 45pp; English.

XX CC Growth of birds is increased by (a) admin. to the bird, in ovo,

XX CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;

XX CC (b) incubating to hatch and (c) growing the birds for at least 3

XX CC weeks after hatch.

XX CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or

XX CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,

XX CC partic. Gly and the Thr normally adjacent to Glu can be replaced

XX CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal

XX CC given in R51439-49.

XX CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced

XX CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent

XX CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.

XX CC comprises the N-terminal given in R51450-53.

XX CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human

XX CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid

XX CC N-terminal extension.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 15; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

DB 3 C 3

RESULT 8

R51441

ID R51441 standard; peptide; 3 AA.

XX AC R51441;

XX DT 27-OCT-1994 (first entry)

XX DE IGF-1 analogue N-terminal.

XX KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;

XX KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.

XX OS Homo sapiens.

XX PN WO9406445-A.

XX PD 31-MAR-1994.

XX PF 02-SEP-1993; 93WO-US08279.

XX PR 17-SEP-1992; 92US-0947035.

XX PA (EMBR-) EMBREX INC.

XX PA (GROP-) GROPEP PTY LTD.

XX PA (USDA) US SEC OF AGRIC.

XX PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;

XX PI Walton PE;

XX WPI; 1994-118144/14.

XX PT Increasing growth of birds - with insulin-like growth factor

XX PT delivered to the egg before hatching esp. for increasing wt. gain

XX PT in chickens.

XX PS Claim 6; Page 37; 45pp; English.

XX CC Growth of birds is increased by (a) admin. to the bird, in ovo,

XX CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;

XX CC (b) incubating to hatch and (c) growing the birds for at least 3

XX CC weeks after hatch.

XX CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or

XX CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,

XX CC partic. Gly and the Thr normally adjacent to Glu can be replaced

XX CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal

XX CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced  
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent  
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.  
 CC comprises the N-terminal given in R51450-53.  
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human  
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid  
 CC N-terminal extension.  
 XX  
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 15; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 C 2  
 Db 3 C 3

RESULT 9  
 W19847  
 ID W19847 standard; Peptide; 3 AA.  
 AC W19847;  
 XX  
 XX 23-SEP-1997 (first entry)  
 XX  
 XX Human interleukin-12 p40 subunit N-terminal peptide.  
 XX  
 XX Interleukin-12; Fc gamma-1; immunosuppressive; autoimmune disease;  
 KW graft rejection; toxic shock; therapy.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9720062-A1.  
 XX  
 XX 05-JUN-1997.  
 XX  
 XX 02-DEC-1996; 96WO-US19181.  
 XX  
 XX 01-DEC-1995; 95US-0565856.  
 PR  
 XX (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
 PA (UTMA-) UNIV MASSACHUSETTS.  
 PA  
 XX Steel AW, Strom TB;  
 XX  
 XX WPI; 1997-310615/28.  
 DR  
 XX N-PSDB; T72095-96.  
 DR  
 XX Fusion protein containing interleukin-12 p40 sub-unit - has  
 PT increased stability, used to inhibit graft rejection, or treat  
 PT autoimmune disease and endotoxin-induced shock  
 XX  
 XX Example; Fig 2; 36pp; English.

CC A peptide (W19847) comprises the three N-terminal amino acid  
 CC residues of human interleukin-12 (IL-12) p40 subunit. It is  
 CC encoded both by native human p40 cDNA (T72096) and by a primer  
 CC (T72095) based on the native sequence. PCR amplification has  
 CC been used to amplify p40 cDNA. A fusion protein comprising the  
 CC p40 subunit and human Fc gamma-1 (see also W19853) was expressed  
 CC in E. coli. This fusion protein has a longer in vivo half-life  
 CC than native p40 and can be used as an immunosuppressive (e.g. to  
 CC treat autoimmune diseases or to inhibit graft rejection) or to  
 CC treat or prevent endotoxin-induced shock.  
 XX  
 XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 18; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 C 2  
 Db 2 C 2

RESULT 10  
 W56231  
 ID W56231 standard; peptide; 3 AA.  
 XX  
 AC W56231;  
 XX  
 XX 20-JUL-1998 (first entry)  
 DT  
 XX Anti-inflammatory tripeptide.  
 DE  
 XX Anti-inflammatory; macrophage inhibitory activity; fibronectin;  
 KW T-cell inhibitory activity; adherence; extracellular matrix;  
 KW up-regulation; fas receptor expression; inflammation.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9809985-A2.  
 XX  
 XX 12-MAR-1998.  
 PD  
 XX 03-SEP-1997; 97WO-IL00295.  
 PF  
 XX 28-MAY-1997; 97US-0864301.  
 PR  
 XX 03-SEP-1996; 96US-0025376.  
 PR  
 XX 20-NOV-1996; 96US-0753141.  
 XX  
 XX (YEDA) YEDA RES & DEV CO LTD.  
 PA  
 XX  
 XX Beserman P, Eisenbachschwartz M, Hirschberg DL;  
 PI WPI; 1998-193550/17.  
 XX  
 XX Anti-inflammatory peptides and derivatives - used for treating, e.g.  
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,  
 PT shock, HIV infection, transplant rejection or Alzheimer's disease  
 XX  
 XX Claim 7; Page 35; 42pp; English.

CC W56171-248 represent anti-inflammatory tripeptides of the invention.  
 CC They are derived from the formulae:  
 CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where  
 CC Xaa = any amino acid residue.  
 CC Cyclic derivatives of the peptides also function as anti-inflammatory  
 CC agents. The peptides can be covalently linked to one another either  
 CC directly or through a spacer. The peptides and their derivatives have  
 CC macrophage inhibitory and T-cell inhibitory activity and thus,  
 CC anti-inflammatory activity. The peptides and compositions have  
 CC anti-immune activity, i.e. inhibitory effects against a cellular and  
 CC humoral immune response, including a response not associated with  
 CC inflammation. The peptides also inhibit the ability of macrophages and  
 CC T-cells to adhere to extracellular matrix components and fibronectin, as  
 CC well as up-regulated fas receptor expression in T-cells. They can be used  
 CC to inhibit unwanted immune reaction and inflammation.  
 XX  
 XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 C 2  
 Db 3 C 3





OS Synthetic.  
XX WO9809985-A2.  
XX  
XX PD 12-MAR-1998.  
XX  
XX PF 03-SEP-1997; 97WO-IL00295.  
XX  
XX PR 28-MAY-1997; 97US-0864301.  
XX PR 03-SEP-1996; 96US-0025376.  
XX PR 20-NOV-1996; 96US-0753141.  
XX  
XX PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;  
XX DR WPI; 1998-193550/17.  
XX  
XX Anti-inflammatory peptides and derivatives - used for treating, e.g.  
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,  
PT shock, HIV infection, transplant rejection or Alzheimer's disease  
XX  
XX Claim 3; Page 34; 42pp; English.  
XX  
XX W56171-248 represent anti-inflammatory tripeptides of the invention.  
CC They are derived from the formulae:  
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where  
CC Xaa = any amino acid residue.  
CC Cyclic derivatives of the peptides also function as anti-inflammatory  
CC agents. The peptides can be covalently linked to one another either  
CC directly or through a spacer. The peptides and their derivatives have  
CC macrophage inhibitory and T-cell inhibitory activity and thus,  
CC anti-inflammatory activity. The peptides and compositions have  
CC anti-immune activity, i.e. inhibitory effects against a cellular and  
CC humoral immune response, including a response not associated with  
CC inflammation. The peptides also inhibit the ability of macrophages and  
CC T-cells to adhere to extracellular matrix components and fibronectin, as  
CC well as up-regulated fas receptor expression in T-cells. They can be used  
CC to inhibit unwanted immune reaction and inflammation.  
XX  
XX Sequence 3 AA;  
SQ

Query Match 75.0%; Score 9; DB 19; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 C 2  
Db 1 C 1  
RESULT 14  
ID W88037  
XX W88037 standard; peptide; 3 AA.  
XX  
XX AC W88037;  
XX  
XX DT 09-APR-1999 (first entry)  
XX  
XX DE Peptide used in the hair composition of the invention.  
XX  
XX KW Hair; styling; wave.  
XX  
XX OS Synthetic.  
XX  
XX PN JP11012138-A.  
XX  
XX PD 19-JAN-1999.  
XX  
XX PF 18-JUN-1997; 97JP-0161657.  
XX

PR 18-JUN-1997; 97JP-0161657.  
XX  
XX PA (LIOY ) LION CORP.  
XX  
XX DR WPI; 1999-148442/13.  
XX  
XX PT New composition for hair - comprises oligopeptide having more than 2  
PT cysteine residues and reducing agent  
XX  
XX PS Example 2; Page 6; 17pp; Japanese.  
XX  
XX CC Peptides W88033-39 are used in the hair composition of the invention.  
CC The specification describes a hair composition that comprises at  
CC least one oligopeptide having more than two cysteine residues and more  
CC than three amino acid residues of the same kind (except cysteine) and a  
CC reducing agent. The composition is useful for styling hair to take  
CC various shapes and waves safely and effectively.  
XX  
XX SQ Sequence 3 AA;  
SQ

Query Match 75.0%; Score 9; DB 20; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 C 2  
Db 1 C 1  
RESULT 15  
ID Y51896  
XX Y51896 standard; peptide; 3 AA.  
XX AC Y51896;  
XX  
XX DT 16-JUN-2000 (first entry)  
XX  
XX DE Biostatin TT232 synthesising peptide 1.  
XX  
XX KW Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor;  
KW cellular proliferation inhibition; somatostatin; antitumor.  
XX  
XX OS Unidentified.  
XX  
XX FH Key Location/Qualifiers  
FT Modified-site 1 /note= "TFA\*Lys(2)"  
FT Modified-site 2 /note= "Cys(Acm)"  
FT Modified-site 3 /note= "Thr(tBu) with C-terminal amide group"  
FT  
XX WO200011032-A2.  
XX  
XX PD 02-MAR-2000.  
XX  
XX PF 20-AUG-1999; 99WO-EP06131.  
XX  
XX PR 20-AUG-1998; 98WO-EP05306.  
XX  
XX PA (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.  
XX  
XX PI Braum G, Liffeith A, Birr C;  
XX  
XX DR WPI; 2000-224663/19.  
XX  
XX PT Biostatin preparation in high yield by solid synthesis, including  
PT closure of disulfide bridge before cleavage from support, useful as  
PT antitumor agent  
XX  
XX PS Example 4; Page 23; 33pp; German.  
XX

CC This invention describes a novel method for the solid phase (SP)  
CC synthesis of biostatin (TT 232) (I) which includes closing the disulfide  
CC bridge by oxidation of the completely or partially constructed peptide  
CC while still bonded to the solid phase. The products of the invention have  
CC cytostatic activity and are tyrosine kinase inhibitors. (I) inhibits the  
CC tyrosine kinase activity of various human stomach cancer cell lines and  
CC thus inhibits cellular proliferation. The heptapeptide (I) described in  
CC the invention is a somatostatin analog which shows strong antitumor  
CC activity in vitro and in vivo. The SP synthesis method gives (I) is more  
CC easily and in markedly higher yield than by the method of EP505680, in  
CC which the cyclization is carried out after cleaving the peptide from the  
CC resin. The solution method is also a simple synthesis of (I) in high  
CC yield; typically the tert-butyl-protected precursor can be oxidized in  
CC a yield of 70-80%. Y51896-Y51900 represent peptides used in the  
CC synthesis of biostatin TT232 described in the method of the invention.

XX  
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 21; Length 3;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
|  
Db 2 C 2

Search completed: February 5, 2001, 12:01:19  
Job time: 366 sec

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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:53 ; Search time 30.91 Seconds  
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2.324 Million cell updates/sec

Title: US-09-687-267-4  
Perfect score: 12  
Sequence: 1 XCXX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2.6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2.6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2.6/ptodata/2/1aa/6\_COMB.pep:\*  
4: /cgn2.6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
5: /cgn2.6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	75.0	2	1	US-07-791-213D-23
2	9	75.0	2	1	US-07-791-213D-39
3	9	75.0	2	1	US-08-133-804-9
4	9	75.0	2	1	US-08-354-240A-12
5	9	75.0	2	1	US-08-461-838-9
6	9	75.0	2	1	US-08-293-150A-23
7	9	75.0	2	1	US-08-293-150A-39
8	9	75.0	2	2	US-08-461-386-9
9	9	75.0	2	2	US-08-465-380-307
10	9	75.0	2	2	US-08-486-397-307
11	9	75.0	2	2	US-08-486-399-307
12	9	75.0	2	2	US-08-461-965-307
13	9	75.0	2	2	US-08-634-641-307
14	9	75.0	2	2	US-08-818-253-52
15	9	75.0	2	3	US-09-249-471-307
16	9	75.0	2	3	US-09-249-472-307
17	9	75.0	2	3	US-09-249-451-307
18	9	75.0	2	3	US-08-809-455-307
19	9	75.0	2	3	US-09-249-461-307
20	9	75.0	2	3	US-09-249-448-307
21	9	75.0	3	1	US-07-791-213D-22
22	9	75.0	3	1	US-07-791-213D-38
23	9	75.0	3	1	US-07-945-982-2
24	9	75.0	3	1	US-07-945-982-8
25	9	75.0	3	1	US-07-947-035-3
26	9	75.0	3	1	US-07-947-035-4
27	9	75.0	3	1	US-07-947-035-5
28	9	75.0	3	1	US-08-285-443-4

29	9	75.0	3	1	US-08-079-812-31	Sequence 31, Appl
30	9	75.0	3	1	US-08-122-510-11	Sequence 11, Appl
31	9	75.0	3	1	US-08-122-510-12	Sequence 12, Appl
32	9	75.0	3	1	US-08-122-510-13	Sequence 13, Appl
33	9	75.0	3	1	US-07-789-913-26	Sequence 26, Appl
34	9	75.0	3	1	US-08-371-930-4	Sequence 4, Appl
35	9	75.0	3	1	US-08-049-794-26	Sequence 26, Appl
36	9	75.0	3	1	US-08-372-455-2	Sequence 2, Appl
37	9	75.0	3	1	US-08-372-455-8	Sequence 8, Appl
38	9	75.0	3	1	US-08-321-585A-1	Sequence 1, Appl
39	9	75.0	3	1	US-08-321-585A-2	Sequence 2, Appl
40	9	75.0	3	1	US-08-321-585A-3	Sequence 3, Appl
41	9	75.0	3	1	US-08-446-908-14	Sequence 14, Appl
42	9	75.0	3	1	US-08-231-205A-14	Sequence 22, Appl
43	9	75.0	3	1	US-08-293-150A-22	Sequence 14, Appl
44	9	75.0	3	1	US-08-293-150A-38	Sequence 38, Appl
45	9	75.0	3	3	US-08-447-515-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-07-791-213D-23  
; Sequence 23, Application US/07791213D  
; Patent No. 5409895  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791,213D  
; FILING DATE: 13-NOV-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-791-213D-23

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      2 C 2
Db      2 C 2

RESULT 2
US-07-791-213D-39
; Sequence 39, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshiro
; APPLICANT: NOSUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-39

Query Match      75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 C 2
Db      1 C 1

RESULT 3
US-08-133-804-9
; Sequence 9, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
```

```
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..2
; OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
US-08-133-804-9

Query Match      75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 C 2
Db      2 C 2

RESULT 4
US-08-354-240A-12
; Sequence 12, Application US/08354240A
; Patent No. 5670356;
; GENERAL INFORMATION:
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Wood, Keith V.
; TITLE OF INVENTION: MODIFIED LUCIFERASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1514
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,240A
; FILING DATE: 12-DEC-1994
; CLASSIFICATION: 435
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ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 34506.029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-831-2100  
TELEFAX: 608-831-2106  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-354-240A-12

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
DB 1 C 1

RESULT 5  
US-08-461-838-9  
Sequence 9, Application US/08461838  
Patent No. 5753204  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
TITLE OF INVENTION: Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/461,838  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..2  
OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"  
US-08-461-838-9

ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 34506.029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-831-2100  
TELEFAX: 608-831-2106  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-354-240A-12

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
DB 1 C 1

RESULT 6  
US-08-293-150A-23  
Sequence 23, Application US/08293150A  
Patent No. 5792629  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TITLE OF INVENTION: TREATING USING THE SAME  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 19-AUG-1994  
APPLICATION NUMBER: US/08/293,150A  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-293-150A-23

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
DB 2 C 2

RESULT 7  
US-08-293-150A-39  
Sequence 39, Application US/08293150A



;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/268  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.  
US-08-465-380-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
|  
Db 1 C 1

RESULT 10  
US-08-486-397-307  
;; Sequence 307, Application US/08486397  
;; Patent No. 5866542  
;; GENERAL INFORMATION:  
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
;; APPLICANT: Peter W. Bergum  
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
;; NUMBER OF SEQUENCES: 357  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION NUMBER: US/08/486,397  
;; FILING DATE: June 5, 1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/269  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.  
US-08-486-397-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
|  
Db 1 C 1

RESULT 11  
US-08-486-399-307  
;; Sequence 307, Application US/08486399  
;; Patent No. 5866543  
;; GENERAL INFORMATION:  
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
;; APPLICANT: Peter W. Bergum  
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
;; NUMBER OF SEQUENCES: 356  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION NUMBER: US/08/486,399  
;; FILING DATE: June 5, 1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/270  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.

US-08-486-399-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
|  
DB 1 C 1

## RESULT 12

US-08-461-965-307  
; Sequence 307, Application US/08461965  
; Patent No. 5872098  
; GENERAL INFORMATION:  
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
; APPLICANT: Joris H.L. Menssens, Marc J. Lauwereys,  
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
; APPLICANT: Peter W. Bergum  
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,965  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 210/243  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; amino acid.  
US-08-461-965-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
|  
DB 1 C 1

## RESULT 13

US-08-634-641-307  
; Sequence 307, Application US/08634641  
; Patent No. 5955294  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George P. Vlasuk  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Menssens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Gansemans, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew  
; APPLICANT: Bergum, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/634,641  
; FILING DATE: April 19, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13231  
; FILING DATE: October 17, 1995  
; APPLICATION NUMBER: 08/486,399  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/486,397  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/465,380  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/461,965  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 219/136  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; amino acid.  
US-08-634-641-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 2 C 2  
|  
Db 1 C 1

## RESULT 14

US-08-818-253-52  
; Sequence 52, Application US/08818253  
; Patent No. 5998204  
; GENERAL INFORMATION:  
; APPLICANT: Tsiens, Roger Y.  
; APPLICANT: Miyawaki, Atsushi  
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
; TITLE OF INVENTION: DETECTION OF ANALITES  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Fastseq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,253  
; FILING DATE: 14-MAR-1997  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Ph.D., Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07257/043001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-818-253-52

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
|  
Db 1 C 1

## RESULT 15

US-09-249-471-307  
; Sequence 307, Application US/09249471  
; Patent No. 6040441  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George Phillip  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Messens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Ganssemans, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew  
; APPLICANT: Berquim, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/249,471  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/809,455  
; FILING DATE: April 17, 1997  
; APPLICATION NUMBER: PCT/US95/13231  
; FILING DATE: October 17, 1995  
; APPLICATION NUMBER: 08/486,399  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/486,397  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/465,380  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/461,965  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 216/270  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; OTHER INFORMATION: amino acid.  
US-09-249-471-307

Query Match 75.0%; Score 9; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
|  
Db 1 C 1

Search completed: February 5, 2001, 12:01:53  
Job time: 335 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2001, 12:02:32 ; Search time 34.92 Seconds  
(without alignments)  
7.778 Million cell updates/sec

Title: US-09-687-267-4

Perfect score: 12

Sequence: 1 XCXX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_66:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	75.0	3	2 A22565	R-phycoerythrin al
2	9	75.0	4	2 I51049	metallothionein-A
3	9	75.0	4	2 S43959	Ig mu chain V regi
4	9	75.0	4	2 S5238	pallidipin - assas
5	9	75.0	5	2 A22565	R-phycoerythrin al
6	9	75.0	5	2 F22565	R-phycoerythrin ga
7	9	75.0	5	2 A33882	cadmium-binding pe
8	9	75.0	5	2 B45525	actin I - malaria
9	9	75.0	5	2 S5726	hemoglobin, extrac
10	9	75.0	6	2 J00355	lipopeptide WS1279
11	9	75.0	6	2 C22565	R-phycoerythrin be
12	9	75.0	6	2 I37027	protamine P1 - gor
13	9	75.0	6	2 I37263	Y protein - human
14	9	75.0	6	2 S29881	Na+/K+-exchanging
15	9	75.0	6	2 H48394	glycoprotein compo
16	9	75.0	6	2 I67345	MHC H2-K-k cell su
17	9	75.0	6	2 I65546	MHC H2-L antigen -
18	9	75.0	6	2 P0652	T-cell receptor be.
19	9	75.0	6	2 P1946	laminin B1 - weste
20	9	75.0	6	2 I49421	hypothetical TC13
21	9	75.0	6	4 I79564	Ig heavy chain V r
22	9	75.0	7	2 P1408	venom heptapeptide
23	9	75.0	7	2 A58512	hypothetical prote
24	9	75.0	7	2 S08606	mabinlin II chain
25	9	75.0	7	2 S38516	vicillin 57K chain
26	9	75.0	7	2 B34818	cadmium-binding he
27	9	75.0	7	2 B33882	acetylcholinestera
28	9	75.0	7	2 A34026	formylglycinamide
29	9	75.0	7	2 A12016	

30 9 75.0 7 2 PH1602 Ig H chain V-D-J r  
31 9 75.0 7 2 PH0932 T-cell receptor be  
32 7 4 I56695 hypothetical I2 pr  
33 9 75.0 8 2 PH1407 Ig heavy chain V r  
34 9 75.0 8 2 S59622 metallothionein is  
35 9 75.0 8 2 XGHUEU urine glycopeptide  
36 9 75.0 8 2 A25836 L-serine dehydrata  
37 9 75.0 8 2 PC1002 leucine--trNA liga  
38 9 75.0 8 2 S19288 acylase - Kluyvera  
39 9 75.0 8 2 A37521 R-phycoerythrin ga  
40 9 75.0 8 2 C61512 variant surface gl  
41 9 75.0 8 2 D61512 variant surface gl  
42 9 75.0 8 2 PH1618 Ig H chain V-D-J r  
43 9 75.0 8 2 PH0803 T-cell receptor al  
44 9 75.0 8 2 I57018 gene Cfr protein  
45 9 75.0 8 2 PH0934 T-cell receptor be

#### ALIGNMENTS

##### RESULT 1

A22565 R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)

C:Species: Gastroclonium coulteri

C>Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993

C:Accession: A22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: A22565

A:Molecule type: protein

A:Residues: 1-3 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
Db 1 C 1

##### RESULT 2

I51049

metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: I51049

R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)

A:Reference number: I51049; MUID:95324545

A:Accession: I51049

A>Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <OLS>

A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 75.0%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
Db 4 C 4

##### RESULT 3

S43959

Ig mu chain V region (clone l3) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
C:Accession: S43959  
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;  
Nucleic Acids Res. 22, 1389-1393, 1994  
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
A:Reference number: S43956; MUID:94248036  
A:Accession: S43959  
A:Molecule type: DNA  
A:Residues: 1-4 <WAG>  
C:Keywords: immunoglobulin

Query Match 75.0%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 2 C 2

RESULT 4

S55238

R-phycocerythrin alpha-2 chain (fragment)

C:Species: Triatoma pallidipennis (assassin bug)

C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000

C:Accession: S55238

R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleuning

Biochem. J. 307, 465-470, 1995

A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib

A:Reference number: S55238; MUID:95251610

A:Accession: S55238

A:Molecule type: protein

A:Residues: 1-4 <HAE>

Query Match 75.0%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 3 C 3

RESULT 5

B22565

R-phycocerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)

C:Species: Gastroclonium coulteri

C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993

C:Accession: B22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycocerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: B22565

A:Molecule type: protein

A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 2 C 2

RESULT 6

F22565

R-phycocerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)  
C:Species: Gastroclonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: F22565  
R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycocerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: F22565

A:Molecule type: protein

A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 3 C 3

RESULT 7

A33882

cadmium-binding pentapeptide - downy thornapple

C:Species: Datura innoxia (downy thornapple)

C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 18-Jun-1993

C:Accession: A33882

R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987

A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plan

A:Reference number: A94182; MUID:88016144

A:Accession: A33882

A:Molecule type: protein

A:Residues: 1-5 <JAC>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 2 C 2

RESULT 8

B45525

actin I - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C:Date: 03-Jun-1993 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000

C:Accession: B45525

R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoc:

Mol. Biochem. Parasitol. 35, 167-176, 1989

A:Title: Stage-specific expression and genomic organization of the actin genes of the

A:Reference number: A45525; MUID:89364996

A:Accession: B45525

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <WES>

A:Cross-references: GB:J03988

A>Note: the authors translated the codon GAA for residue 3 as Gly

C:Comment: The actin I gene contains no introns.

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 4 C 4

RESULT 9  
S65726  
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)  
C:Species: Lumbricus terrestris (common earthworm)  
C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65726  
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.  
Biochim. Biophys. Acta 1292, 273-280, 1996  
A>Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A:Reference number: S65721; MUID:96176855  
A:Accession: S65726  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <FUS>

Query Match 75.0%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 C 2  
|  
Db 4 C 4

RESULT 10  
JU0355  
lipopeptide WSL279 [validated] - Streptomyces willmorei  
C:Species: Streptomyces willmorei  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: JU0355  
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.  
Chem. Pharm. Bull. 39, 607-611, 1991  
A>Title: Structure and synthesis of an immunoreactive lipopeptide, WSL279, of microbial origin  
A:Reference number: JU0355; MUID:91300586  
A:Accession: JU0355  
A:Molecule type: protein  
A:Residues: 1-6 <TSU>  
A>Note: the structure was confirmed by synthesis  
C:Keywords: blocked amino end; lipoprotein  
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental  
F:1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 C 2  
|  
Db 1 C 1

RESULT 11  
C22565  
R-phycocerythrin beta-1 chain - red alga (Gastrocloonium coulteri) (fragment)  
C:Species: Gastrocloonium coulteri  
C>Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: C22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A>Title: Characterization of the bilin attachment sites in R-phycocerythrin.  
A:Reference number: A22565; MUID:85182601  
A:Accession: C22565  
A:Molecule type: protein  
A:Residues: 1-6 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 C 2  
|  
Db 4 C 4

RESULT 12  
I37027  
protamine P1 - gorilla (fragment)  
C:Species: Gorilla gorilla (gorilla)  
C>Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jul-2000  
C:Accession: I37027  
R:Queralt, R.; Oliiva, R.  
Gene 133, 197-204, 1993  
A>Title: Identification of conserved potential regulatory sequences of the protamine-c  
A:Reference number: I37013; MUID:94040810  
A:Accession: I37027  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 C 2  
|  
Db 6 C 6

RESULT 13  
I37263  
Y protein - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I37263  
R:Waechter, G.; Habener, J.F.  
Endocrinology 131, 2010-2015, 1992  
A>Title: Novel testis germ cell-specific transcript of the CREB gene contains an alt  
A:Reference number: I37263; MUID:93010691  
A:Accession: I37263  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816  
C:Genetics:  
A:Gene: CREB

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 C 2  
|  
Db 4 C 4

RESULT 14  
S29881  
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 07-May-1999  
C:Accession: S29881  
R:Waelderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.  
J. Biol. Chem. 260, 3852-3859, 1985  
A>Title: Structural relatedness of three ion-transport adenosine triphosphatases arou  
A:Reference number: S29881; MUID:85131201  
A:Accession: S29881  
A:Molecule type: protein  
A:Residues: 1-6 <WAL>  
A:Experimental source: kidney

C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;  
F:4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
I  
Db 2 C 2

## RESULT 15

H48394  
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C:Accession: H48394  
R:Mather, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
II-like sequences.  
A:Reference number: A48394; MUID:93250576  
A:Accession: H48394  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6 <MAT>  
A:Experimental source: milk  
A>Note: sequence extracted from NCBI backbone (NCBIP:131518)  
C:Keywords: glycoprotein

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
I  
Db 6 C 6

Search completed: February 5, 2001, 12:02:32  
Job time: 289 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2001, 12:06:02 ; Search time 20.72 Seconds  
(without alignments)  
6.234 Million cell updates/sec

Title: US-09-687-267-4  
Perfect score: 12  
Sequence: 1 XCXX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	9	75.0	8 1 ACT_CARMA	P80709 carcinus ma
2	9	75.0	8 1 GLUR_HUMAN	P02729 homo sapien
3	9	75.0	9 1 CCAP_CARMA	P38556 carcinus ma
4	9	75.0	9 1 CONO_CONGE	P05486 conus geogr
5	9	75.0	9 1 CONO_CONST	P05487 conus stria
6	9	75.0	9 1 DNF1_LOCXI	P16339 locusta mig
7	9	75.0	9 1 ISOT_CYPCA	P42993 cyprinus ca
8	9	75.0	9 1 MGMT_BOVIN	P29177 bos taurus
9	9	75.0	9 1 OXYA_SCYCA	P42996 scyllorhinu
10	9	75.0	9 1 OXYA_SQUAC	P42997 scyllorhinu
11	9	75.0	9 1 OXYF_SCYCA	P42995 bufo regula
12	9	75.0	9 1 OXYT_BUFRE	P23879 cyprinus ca
13	9	75.0	9 1 OXYT_CYPCA	P42998 eisenia foe
14	9	75.0	9 1 OXYT_EISFO	P80027 octopus vul
15	9	75.0	9 1 OXYT_OCTVU	P32878 oryctolagus
16	9	75.0	9 1 OXYT_RABIT	P42994 raja clavata
17	9	75.0	9 1 OXYT_RAJCL	P43000 squalus aca
18	9	75.0	9 1 OXYT_SQUAC	OS4296 salmoneilla
19	9	75.0	9 1 RS11_SALTY	P24047 stomopneute
20	9	75.0	9 1 SAP_STOVA	P17440 pichia jadi
21	9	75.0	9 1 TAL1_PICJA	P17441 pichia jadi
22	9	75.0	9 1 TAL3_PICJA	P02728 homo sapien
23	9	75.0	10 1 GLEM_HUMAN	P80678 cheilosoma
24	9	75.0	10 1 GONZ_CHEPR	P81084 pinus pinas
25	9	75.0	10 1 RCA_PINPS	P50983 conus imper
26	9	75.0	12 1 CXAL_CONIM	O22426 lotus japon
27	9	75.0	12 1 NO40_LOTJA	O24369 sesbania ro
28	9	75.0	12 1 NO40_SESRO	P55960 glycine max
29	9	75.0	12 1 NO40_SOYEN	P36207 ginkgo billo
30	9	75.0	12 1 RR16_GINBI	P01371 tremella me
31	9	75.0	12 1 TAL0_TREME	P04558 catostomus
32	9	75.0	12 1 UR2A_CATCO	P04559 catostomus
33	9	75.0	12 1 UR2B_CATCO	

34	9	75.0	12 1 UR2B_CYPCA	P04561 cyprinus ca
35	9	75.0	12 1 UR2_GILMI	P01147 gillioichthys
36	9	75.0	12 1 UR2_POLSP	P81022 polyodon sp
37	9	75.0	12 1 UR2_SCYCA	P35490 scyllorhinu
38	9	75.0	12 1 YZPY_ECOLI	P17776 escherichia
39	9	75.0	13 1 ACT7_SOYBN	P15987 glycine max
40	9	75.0	13 1 CXAL_CONST	P15471 conus stria
41	9	75.0	13 1 CXA2_CONGE	P01520 conus geogr
42	9	75.0	13 1 CXA2_CONST	P28878 conus stria
43	9	75.0	13 1 CXET_CONTE	P81755 conus texti
44	9	75.0	13 1 GER1_HORVU	P28525 hordeum vul
45	9	75.0	13 1 GER2_HORVU	P28526 hordeum vul

#### ALIGNMENTS

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RESULT 1
ACT_CARMA          STANDARD;          PRT;          8 AA.
ID ACT_CARMA
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN (FRAGMENT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32(1996).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 KDA.
CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
CC INTERPRO: IPR000279;
DR PROSITE: PS00405; ACTINS_1; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;
```

Query Match 75.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
DB 2 C 2

```
RESULT 2
GLUR_HUMAN          STANDARD;          PRT;          8 AA.
ID GLUR_HUMAN
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE URINE GLYCOPETIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
```

RP SEQUENCE.  
RX MEDLINE=72062338; PubMed=5126885;  
RA Lote C.J., Weiss J.B.;  
RT "Identification in urine of a low-molecular-weight highly polar  
RT glycopeptide containing cysteinyl-galactose.";  
RL Biochem. J. 123:25p-25P(1971).  
CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE  
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN  
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A  
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.  
DR PIR: A03188; XGHUEU.  
KW Glycoprotein.  
FT CARBOHYD  
SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;  
  
Query Match 75.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 C 2  
|  
Db 1 C 1  
  
RESULT 3  
CCAP\_CARMA  
ID CCAP\_CARMA STANDARD; PRT; 9 AA.  
AC P38556;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CARDIOACTIVE PEPTIDE (CCAP).  
OS Carcinus maenas (Common shore crab) (Green crab),  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),  
OS Tenebrio molitor (Yellow mealworm), and  
OS Spodoptera eridania (Southern armyworm).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C. MAENAS; TISSUE=PERICARDIAL ORGANS;  
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;  
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
RT shore crab Carcinus maenas.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=M. SEXTA;  
RX MEDLINE=93050243; PubMed=1426284;  
RA Cheung C.C., Loi P.K., Sylvester A.W., Lee T.D., Tublitz N.J.;  
RT "Primary structure of a cardioactive neuropeptide from the tobacco  
RT hawkmoth, Manduca sexta.";  
RL FEBS Lett. 313:165-168(1992).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=T. MOLITOR, AND S. ERIDANIA; TISSUE=HEAD;  
RX MEDLINE=94176032; PubMed=8129851;  
RA Furuoya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,  
RA Schooley D.A.;  
RT "Isolation and identification of a cardioactive peptide from Tenebrio  
RT molitor and Spodoptera eridania.";  
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).  
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.  
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
CC INTO THE HEMOLYMPH.  
DR PIR: A26363; A26363.  
DR PIR: A27233; S27233.  
KW Neuropeptide; Amidation.  
FT DISULFID 3 9  
MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 C 2  
|  
Db 3 C 3  
  
RESULT 4  
CONO\_CONGE  
ID CONO\_CONGE STANDARD; PRT; 9 AA.  
AC P05486;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE LYS-CONOPRESSIN G.  
OS Conus geographus (Geography cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88058932; PubMed=3680228;  
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
RA Gray W.R., Olivera B.M.;  
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of  
RT peptides from Conus geographus and Conus straitus venoms.";  
RL J. Biol. Chem. 262:15821-15824(1987).  
RN [2]  
RP REVIEW.  
RX MEDLINE=89024586; PubMed=3052286;  
RA Gray W.R., Olivera B.M., Cruz L.J.;  
RT "Peptide toxins from venomous Conus snails.";  
RL Annu. Rev. Biochem. 57:665-700(1988).  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR: A28495; A28495.  
DR INTERPRO: IPR000981;  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;  
  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 C 2  
|  
Db 1 C 1  
  
RESULT 5  
CONO\_CONST  
ID CONO\_CONST STANDARD; PRT; 9 AA.  
AC P05487;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ARG-CONOPRESSIN S.  
OS Conus striatus (Striated cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88058932; PubMed=3680228;  
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
RA Gray W.R., Olivera B.M.;  
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of



RT peptides from Conus geographus and Conus straitus venoms.";  
 RL J. Biol. Chem. 262:15821-15824(1987).  
 RN [2]

RP REVIEW.  
 RX MEDLINE=89024586; PubMed=3052286;  
 RA Gray W.R., Olivera B.M., Cruz L.J.;  
 RT "Peptide toxins from venomous Conus snails.";  
 RL Annu. Rev. Biochem. 57:665-700(1988).  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR: B28495; B28495.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9  
 FT SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
 DB 1 C 1

RESULT 6  
 DNFL\_LOCM1 STANDARD; PRT; 9 AA.

AC P16339;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE LOCUPRESSIN (DIURETIC NEUROPEPTIDE F1/F2).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;  
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=SUBESOPHAGEAL GANGLION, AND THORACIC GANGLION;  
 RX MEDLINE=88077077; PubMed=3689410;  
 RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,  
 RA Delaage M., Schooley D.A.;  
 RT "Identification of an arginine vasopressin-like diuretic hormone from  
 RT Locusta migratoria.";  
 RL Biochem. Biophys. Res. Commun. 149:180-186(1987).  
 CC -!- FUNCTION: DIURETIC HORMONE.  
 CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

PIR: A29477; A29477.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Neuropeptide; Amidation.  
 FT DISULFID 1 6  
 FT DISULFID 1 1  
 FT DISULFID 6 6  
 FT MOD\_RES 9 9  
 FT SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
 DB 1 C 1

RESULT 7  
 ISOT\_CYPCA STANDARD; PRT; 9 AA.

ID ISOT\_CYPCA  
 AC P42993;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE ISOTOCIN.  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=PIUITARY;  
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
 RT "Characterization of neurohypophyseal hormones from a fresh water bony  
 RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea  
 RT water bony fish.";  
 RL Comp. Biochem. Physiol. 14:245-254(1965).  
 CC -!- FUNCTION: ANTIDIURETIC HORMONE.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

PIR: A61364; A61364.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9  
 FT SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
 DB 1 C 1

RESULT 8  
 MGMT\_BOVIN STANDARD; PRT; 9 AA.

ID MGMT\_BOVIN  
 AC P29177;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) (FRAGMENT).  
 GN MGMT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=THYMUS;  
 RX MEDLINE=90174912; PubMed=2308822;  
 RA Rydberg B., Hall J., Karren P.;  
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA  
 RT methyltransferase.";  
 RL Nucleic Acids Res. 18:17-21(1990).

CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY  
 CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE  
 CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS  
 CC IRREVERSIBLY INACTIVATED.  
 CC -!- CATALYTIC ACTIVITY: DNA (CONTAINING O6-METHYLGUANINE) + PROTEIN  
 CC L-CYSTEINE -> DNA (WITHOUT O6-METHYLGUANINE) + PROTEIN S-METHYL-  
 CC L-CYSTEINE.  
 CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE  
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.  
 DR INTERPRO: IPR001497; -.

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DR PROSITE: PS00374; MGMT: PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 9 C 9

RESULT 9
OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PIUITARY;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: aspartocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 1 C 1

RESULT 10
OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN (ASPARTOCIN).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;

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RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

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Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 1 C 1

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RESULT 11
OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHASVATOCIN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PIUITARY;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: aspartocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

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Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 1 C 1

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RESULT 12
OXYT_BUFRE

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ID OXYT\_BUFE STANDARD; PRT; 9 AA.  
AC P42995;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE SERITOCIN.  
OS Bufo regularis (African toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;  
OC Bufo.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=PITUITARY NEUROINTERMEDIATE LOBE;  
RX MEDLINE=96059313; PubMed=7591488;  
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;  
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),  
RT identified in a dryness-resistant African toad, Bufo regularis.";  
RL Int. J. Pept. Protein Res. 45:482-487(1995).  
CC -!- FUNCTION: DEVOID OF OXYTOCIN ACTIVITY.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR INTERPRO: IPR000981; -;  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
FT SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;  
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 C 2  
Db 1 C 1  
RESULT 13  
OXYT\_CYPCA  
ID OXYT\_CYPCA STANDARD; PRT; 9 AA.  
AC P23879;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE VASOTOCIN.  
OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C.CARPIO; TISSUE=PITUITARY;  
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
RT "Characterization of neurohypophyseal hormones from a fresh water bony  
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea  
RT water bony fishs.";  
RL Comp. Biochem. Physiol. 14:245-254(1965).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=P.MARINUS; TISSUE=PITUITARY;  
RX MEDLINE=88225976; PubMed=3371648;  
RA Lane T.F., Sower S.A., Kawauchi H.;  
RT "Arginine vasotocin from the pituitary gland of the lamprey  
RT (Petromyzon marinus): isolation and amino acid sequence.";  
RL Gen. Comp. Endocrinol. 70:152-157(1988).  
CC -!- FUNCTION: ANTIDIURETIC HORMONE.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR; B61364; B61364.  
DR INTERPRO: IPR000981; -;  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.

KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
FT SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;  
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 C 2  
Db 1 C 1  
RESULT 14  
OXYT\_EISFO  
ID OXYT\_EISFO STANDARD; PRT; 9 AA.  
AC P42998;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ANNETOCIN.  
OS Eisenia foetida (Common branding worm) (Common dung-worm).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;  
OC Lumbricina; Lumbricidae; Eisenia.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=PITUITARY;  
RX MEDLINE=94121660; PubMed=8292046;  
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,  
RA Nemoto K.;  
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,  
RT Eisenia foetida.";  
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).  
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO  
CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE  
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH  
CC NEPHRIDIAL FUNCTION.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR; PC2021; PC2021.  
DR INTERPRO: IPR000981; -;  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
FT SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;  
SQ SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 C 2  
Db 1 C 1  
RESULT 15  
OXYT\_OCTVU  
ID OXYT\_OCTVU STANDARD; PRT; 9 AA.  
AC P80027;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CEPHALOTOCIN.  
OS Octopus vulgaris (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;  
OC Incirrata; Octopodidae; Octopus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=NERVE ENDINGS;

RX MEDLINE-92270139; PubMed-1589145;  
RA Reich G.;  
RT "A new peptide of the oxytocin/vasopressin family isolated from  
RT nerves of the cephalopod Octopus vulgaris.";  
RL Neurosci. Lett. 134:191-194(1992).  
CC -!- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA  
CC CAVA.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR INTERPRO: IPR000981; -.  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1072 MW; 17FF476BA5409DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 C 2  
Db 1 C 1

Search completed: February 5, 2001, 12:06:02  
Job time: 279 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:05:38 ; Search time 57.72 Seconds  
(without alignments)  
8.123 Million cell updates/sec

Title: US-09-687-267-4  
Perfect score: 12  
Sequence: 1 XCXX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_15:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mmc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	6	Q08720	Q08720 homo sapien
2	9	75.0	7	P70804	P70804 azotobacter
3	9	75.0	7	O55184	O55184 rattus norv
4	9	75.0	7	Q66113	Q66113 cherry leaf
5	9	75.0	7	Q67113	Q67113 influenza a
6	9	75.0	7	Q9YVE3	Q9YVE3 human adeno
7	9	75.0	7	Q9YI90	Q9YI90 human adeno
8	9	75.0	7	Q9YI09	Q9YI09 human adeno
9	9	75.0	7	Q42564	Q42564 figu rubrip
10	9	75.0	8	O32560	O32560 escherichia
11	9	75.0	8	Q15888	Q15888 homo sapien
12	9	75.0	8	Q15890	Q15890 homo sapien
13	9	75.0	8	Q15900	Q15900 homo sapien
14	9	75.0	8	Q9Y4X6	Q9Y4X6 homo sapien
15	9	75.0	8	O02831	O02831 oryctolagus
16	9	75.0	8	Q9TRY3	Q9TRY3 sus sp. ins
17	9	75.0	8	Q9SAY7	Q9SAY7 dioscorea t
18	9	75.0	8	P70243	P70243 mus musculu
19	9	75.0	8	O35835	O35835 rattus norv

20	9	75.0	8	12	Q85562	Q85562 moloney mur
21	9	75.0	8	13	Q90493	Q90493 eopsaltria
22	9	75.0	8	13	Q90498	Q90498 erythrura g
23	9	75.0	8	13	Q91098	Q91098 manorina me
24	9	75.0	9	2	Q47063	Q47063 escherichia
25	9	75.0	9	4	Q15999	Q15999 homo sapien
26	9	75.0	9	4	Q99887	Q99887 homo sapien
27	9	75.0	9	6	Q9XT05	Q9XT05 macropus ru
28	9	75.0	9	6	Q9TUY0	Q9TUY0 monodelphis
29	9	75.0	9	9	Q38340	Q38340 lactococcus
30	9	75.0	9	11	Q9QZ88	Q9QZ88 mus musculu
31	9	75.0	9	11	P97889	P97889 rattus norv
32	9	75.0	9	12	Q69473	Q69473 human herpe
33	9	75.0	9	12	O12096	O12096 caprine art
34	9	75.0	9	12	O12098	O12098 caprine art
35	9	75.0	9	12	O12100	O12100 caprine art
36	9	75.0	9	12	O12102	O12102 caprine art
37	9	75.0	9	12	O12104	O12104 caprine art
38	9	75.0	9	12	O90350	O90350 hepatitis g
39	9	75.0	10	2	Q50032	Q50032 mycobacteri
40	9	75.0	10	2	Q47475	Q47475 escherichia
41	9	75.0	10	2	Q48469	Q48469 klebsiella
42	9	75.0	10	2	Q9K343	Q9K343 escherichia
43	9	75.0	10	3	Q9YVW2	Q9YVW2 schizophyll
44	9	75.0	10	4	Q13318	Q13318 homo sapien
45	9	75.0	10	4	Q9UN90	Q9UN90 homo sapien

#### ALIGNMENTS

RESULT 1

Q08720 PRELIMINARY; PRT; 6 AA.  
AC Q08720; PRELIMINARY; PRT; 6 AA.  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Y PROTEIN (FRAGMENT).  
GN CREB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93010691; PubMed=1396344;  
RA Waeber G., Habener J.F.;  
RT "Novel testis germ cell-specific transcript of the CREB gene contains  
RT an alternatively spliced exon with multiple in-frame stop codons."  
RL Endocrinology 131:2010-2015(1992).  
DR EMBL; X68994; CAA48780.1; -.  
FT NON\_TER 1  
FT NON\_TER 6  
SQ SEQUENCE 6 AA: 695 MW: 67272EB9C735D000 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 4 C 4

RESULT 2

P70804 PRELIMINARY; PRT; 7 AA.  
ID P70804  
AC P70804;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE ALG GENE (FRAGMENT).  
GN ALGT.  
OS Azotobacter vinelandii.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Azotobacter.  
OX NCBI\_TaxID=354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E;  
RX MEDLINE=96427318; PubMed=8830682;  
RA Rehm B.H.A., Ertesvag H., Valla S.;  
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is  
RT part of an alg gene cluster physically organized in a manner similar  
RT to that in Pseudomonas aeruginosa.";  
RL J. Bacteriol. 178:5884-5889(1996).  
DR EMBL; X87973; CAA61230.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;  
  
Query Match 75.0%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 C 2  
DB 1 C 1  
  
RESULT 3  
O55184 PRELIMINARY; PRT; 7 AA.  
AC O55184;  
DT 01-JUN-1998 (TReMBLrel. 06, Created)  
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE ORPHAN RECEPTOR TR4-NS (FRAGMENT).  
GN TR4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96198747; PubMed=8612486;  
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,  
RA Detera-Wadleigh S.D.;  
RT "Splice variants of rat TR4 orphan receptor: differential expression  
RT of novel sequences in the 5'-untranslated region and C-terminal  
RT domain.";  
RL Endocrinology 137:1562-1571(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96299786; PubMed=8661150;  
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;  
RT "New variants of the human and rat nuclear hormone receptor, TR4:  
RT expression and chromosomal localization of the human gene.";  
RL Genomics 35:361-366(1996).  
DR EMBL; U59454; AAB91433.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 75.0%; Score 9; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 C 2  
DB 3 C 3  
  
RESULT 4

Q66113 PRELIMINARY; PRT; 7 AA.  
AC Q66113;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE C-TERMINUS OF THE VIRAL REPLICASE (FRAGMENT).  
OS cherry leaf roll virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;  
OC Nepovirus.  
OX NCBI\_TaxID=12615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WALNUT;  
RA Borja M.;  
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WALNUT;  
RX MEDLINE=96124520; PubMed=8560786;  
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;  
RT "Long, nearly identical untranslated sequences at the 3' terminal  
RT regions of the genomic RNAs of cherry leafroll virus (walnut  
RT strain).";  
RL Virus Genes 10:245-252(1995).  
DR EMBL; Z34265; CAA84019.1; -.  
KW Repeat.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 C 2  
DB 4 C 4

RESULT 5  
Q67113 PRELIMINARY; PRT; 7 AA.  
AC Q67113;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE (UDORN/72) HEMAGGLUTININ (SEG 4) CDNA, 3' END (FRAGMENT).  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81001892; PubMed=7407922;  
RA Dhar R., Chanock R.M., Lai C.J.;  
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza  
RT viral mRNA deduced from cloned complete genomic sequences.";  
RL Cell 21:495-500(1980).  
DR EMBL; M25045; AAA43202.1; -.  
KW Hemagglutinin.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 C 2  
DB 3 C 3

```

RESULT 6
Q9YVE3 PRELIMINARY; PRT; 7 AA.
AC Q9YVE3;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_Taxid=10519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GOMEN;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065065; AAD03662.1; -
DR EMBL; AF065065; AAD03662.1; -
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 6 C 6

RESULT 7
Q9YI90 PRELIMINARY; PRT; 7 AA.
AC Q9YI90;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7a.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_Taxid=85755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KN T96-0620, S-1058, CL 68578;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065068; AAD03668.1; -
DR EMBL; AF065066; AAD03664.1; -
DR EMBL; AF065067; AAD03666.1; -
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 6 C 6

RESULT 8
Q9YIQ9 PRELIMINARY; PRT; 7 AA.
AC Q9YIQ9;

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DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 4.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_Taxid=28280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z-G 95-873, RI-67, 55142;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03659.1; -
DR EMBL; AF065062; AAD03653.1; -
DR EMBL; AF065063; AAD03656.1; -
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 6 C 6

RESULT 9
O42564 PRELIMINARY; PRT; 7 AA.
ID O42564;
AC O42564;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT (FRAGMENT).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_Taxid=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -
FT IONIC CHANNEL.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 75.0%; Score 9; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 5 C 5

RESULT 10
O32560 PRELIMINARY; PRT; 8 AA.
ID O32560;
AC O32560;
DT 01-JAN-1998 (TREMBlrel. 05, Created)

```

DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)  
DT 01-AUG-1998 (TREMELrel. 07, Last annotation update)  
DE PROPIONATE KINASE (FRAGMENT).  
GN TDCD.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W3110;  
RA Hesslinger C., Savers G.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ001620; CAA04875.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
DB 6 C 6

RESULT 11  
Q15888 PRELIMINARY; PRT; 8 AA.  
AC Q15888  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMELrel. 07, Last annotation update)  
DE (CLONE XP15H8A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32069; AAA73878.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
DB 5 C 5

RESULT 12  
Q15890 PRELIMINARY; PRT; 8 AA.  
AC Q15890  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMELrel. 07, Last annotation update)

DE (CLONE XP19G12A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32083; AAA73880.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
DB 4 C 4

RESULT 13  
Q15900 PRELIMINARY; PRT; 8 AA.  
AC Q15900  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMELrel. 07, Last annotation update)  
DE (CLONE XP7B11A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32079; AAA73890.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAEB1 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2  
DB 2 C 2

RESULT 14  
Q9Y4X6 PRELIMINARY; PRT; 8 AA.  
AC Q9Y4X6  
DT 01-NOV-1999 (TREMELrel. 12, Created)  
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
DE NUCLEAR LIM INTERACTOR (FRAGMENT).  
GN NLI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.



```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
RA Schroth A., Bodem J., Royer-Pokora B.;
RT "Genomic structure, alternative transcripts and chromosomal
RT localization of the human LIM domain binding protein 1 gene
RT LDB1/NLI."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243097; CAB45408.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 767 MW; EE6EBDEB862D5B6 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 5 C 5

RESULT 15
002831 PRELIMINARY; PRT; 8 AA.
AC O02831;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage."
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; -
FT NON_TER 1
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 75.0%; Score 9; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 4 C 4

Search completed: February 5, 2001, 12:05:38
Job time: 289 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:19 ; Search time 42.35 Seconds  
(without alignments)  
3.230 Million cell updates/sec

Title: US-09-687-267-5

Perfect score: 12

Sequence: 1 XXCX 4

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	3	P10301	Sequence which cor
2	9	75.0	3	P90382	Binding receptor w
3	9	75.0	3	P91660	Synthetic peptide
4	9	75.0	3	R34022	Metal trapping pep
5	9	75.0	3	R34023	Metal trapping pep
6	9	75.0	3	R51439	IGF-1 analogue N-t
7	9	75.0	3	R51440	IGF-1 analogue N-t
8	9	75.0	3	R51441	IGF-1 analogue N-t
9	9	75.0	3	W19847	Human interleukin-
10	9	75.0	3	W56231	Anti-inflammatory
11	9	75.0	3	W56211	Anti-inflammatory
12	9	75.0	3	W56200	Anti-inflammatory

13	9	75.0	3	19	W56172	Anti-inflammatory
14	9	75.0	3	20	W88037	Peptide used in th
15	9	75.0	3	21	W51896	Biostatin TR232 sy
16	9	75.0	4	2	P10138	Sequence of antin
17	9	75.0	4	2	P10093	Sequence of peptid
18	9	75.0	4	2	P10382	Enkephalin-like an
19	9	75.0	4	3	P20217	Analgesic and neur
20	9	75.0	4	4	P30083	Sequence of chromo
21	9	75.0	4	4	P30085	Sequence of cyclic
22	9	75.0	4	5	P40538	Sequence of cyclic
23	9	75.0	4	5	P40539	Sequence of cyclic
24	9	75.0	4	8	P70833	Sequence encoded b
25	9	75.0	4	10	P91661	Synthetic peptide
26	9	75.0	4	12	R11077	Peptide fragment #
27	9	75.0	4	12	R11079	Peptide fragment #
28	9	75.0	4	12	R11508	Thioredoxin active
29	9	75.0	4	12	R11744	Cyclic platelet ag
30	9	75.0	4	12	R11745	Cyclic platelet ag
31	9	75.0	4	12	R12554	Ocular pressure re
32	9	75.0	4	12	R13935	Antibiotic FR90137
33	9	75.0	4	12	R14723	Farnesyl-protein t
34	9	75.0	4	12	R15751	Farnesyl-protein t
35	9	75.0	4	12	R15752	Farnesyl-protein t
36	9	75.0	4	12	R15753	Farnesyl-protein t
37	9	75.0	4	12	R15754	Farnesyl-protein t
38	9	75.0	4	12	R15755	Farnesyl-protein t
39	9	75.0	4	12	R15756	Farnesyl-protein t
40	9	75.0	4	12	R15757	Farnesyl-protein t
41	9	75.0	4	12	R15758	Farnesyl-protein t
42	9	75.0	4	12	R15759	Farnesyl-protein t
43	9	75.0	4	12	R15760	Farnesyl-protein t
44	9	75.0	4	12	R15761	Farnesyl-protein t
45	9	75.0	4	21	Y80840	Fluorophore-label

#### ALIGNMENTS

RESULT 1  
P10301  
ID P10301 standard; Protein; 3 AA.  
XX  
AC P10301;  
DT 19-AUG-1992 (first entry)  
XX  
DE Sequence which corresp. to residues 19-21 of insulin A chain.  
XX  
KW Cystine peptide; insulin activity; hormone; diabetes therapy;  
KW antidiabetic agent.  
XX  
OS Mammal.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 2  
FT /note= "bonded to Cys(5) of P10115, which is  
FT residue 19 of the B chain fragment  
FT B15-27"  
XX  
PN DD147942-A.  
XX  
PD 29-APR-1981.  
XX  
PF 01-FEB-1980; 80DD-0011868.  
XX  
PR 20-AUG-1979; 79DD-0215100.  
XX  
PA (LOSS/) LOSSE G.  
XX  
PI Losse G, Stange H;  
XX  
DR WPI; 1981-53498D/30 (53498D).  
XX

PT Cysteine peptide(s) with antidiabetic activity - contg. fragments  
 PS of insulin A and B chains

XX Claim 1; Page 10; 11pp; German.

CC The inventors claim the prepn. of new cysteine peptides with insulin-like activity. The new peptides comprise a sequence with corresp. to a central portion of the insulin B chain (esp. B15-27) and a cysteine-contg. peptide with an AA sequence corresp. to a terminal portion of the insulin A chain (esp. A1-7). The new cysteine peptides are antidiabetic agents with appreciable insulin activity (lower than that of insulin itself) and low antigenic activity.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
 I  
 Db 2 c 2

RESULT 2

P90982  
 ID P90982 standard; peptide; 3 AA.

XX AC P90982;

XX DT 06-JUN-1990 (first entry)

XX DE Binding receptor with selectivity for a target ligand, borne by an article for inactivating toxic materials.

XX KW Toxic material; inactivator; organophosphorous cpds.; nerve poison; pesticide; decontaminant; military.

XX PN WO8902920-A.

XX PD 06-APR-1989.

XX PF 04-OCT-1988; 88WO-US03422.

XX PR 05-OCT-1987; 87US-0105312.

XX PA (LITT ) LITTLE AD INC.

XX PI Taylor RF;

XX DR WPI; 1989-114395/15.

XX PT Article for inactivating toxic materials, eg organo-phosphorous cpds. - comprises solid carrier bearing target ligand binding receptor and ligand-degrading receptor, pref. enzyme

XX PS Claim 7a; page 42; 57pp; English.

XX CC The article for inactivating a toxic material comprises a solid carrier bearing a first receptor which binds the target ligand and a second receptor which degrades the target ligand. This synthetic peptide is a preferred first receptor. The article may be used for covering surfaces to protect or decontaminate the surface. The article is esp. for degrading toxic organic cpds., esp. organophosphorous cpds., (eg pesticides and nerve poisons, bacteria and viruses, in environmental, chemical, military and industrial settings.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 C 3  
 I  
 Db 2 c 2

RESULT 3

ID P91660 standard; protein; 3 AA.

XX AC P91660;

XX DT 29-JUN-1990 (first entry)

XX DE Synthetic peptide corresp. to residues 12-14 of naturally occurring epidermal growth factor (EGF).

XX KW Epidermal growth factor; angiogenesis; synthetic peptide.

XX FH Key  
 FT Misc-difference 1 Location/Qualifiers  
 FT /label=OTHER  
 FT /note="H-Gly"

FT Misc-difference 3  
 FT /label=OTHER  
 FT /note="(aceto amido methyl) NH2-Cys"

XX PN WO8901489-A.

XX PD 23-FEB-1989.

XX PF 10-AUG-1988; 88WO-AU00300.

XX PR 10-AUG-1987; 87AU-0003629.

XX PA (CSIR ) COMMONWEALTH SCIENT ORG.

XX PI MCAuslan BR;

XX DR WPI; 1989-068852/09.

XX PT Synthetic peptide active in stimulating angiogenesis - has sequences corresponding to amino acid sequences occurring in epidermal growth factor.

XX PS Claim 3; page 10; 11pp; English.

XX CC The inventors claim synthetic peptides which correspond to sequences occurring in EGF, but excluding EGF. The peptides are angiogenic and have corresp. applications, eg for the healing of wounds and burns. Their relative shortness means that they pose fewer synthesis problems than the entire EGF molecule. They can be admin. singly or in association with each other or in association with an angiogenic stimulator.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3

I  
 Db 3 c 3

RESULT 4

ID R34022 standard; peptide; 3 AA.

XX AC R34022;

XX 19-MAY-1993 (first entry)  
 XX Metal trapping peptide intermediate.  
 XX Electrostatic interaction; metalloprotein; binding site;  
 KW protecting group.  
 XX Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site 2 /note= "Boc protected"  
 FT Modified-site 3 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH  
 FT Modified-site 3 of cysteine"  
 FT Modified-site 3 /note= "OME protected"  
 PN JP04346999-A.  
 XX  
 XX 02-DEC-1992.  
 PD  
 XX 24-MAY-1991; 91JP-0120196.  
 PF  
 XX 24-MAY-1991; 91JP-0120196.  
 PR  
 XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.  
 PA  
 XX WPI; 1993-021449/03.  
 DR  
 XX New acyclic peptide with metal trapping activity - exhibits in  
 PT vivo metal transporting action and can be used as drug,  
 PT diagnostic agent or functional material  
 XX  
 PS Claim 3; Page 2; 9pp; Japanese.  
 CC The acyclic peptide (see R31340) with metal trapping activity may be  
 CC produced by fragment condensation using the peptide fragments given in  
 CC R34022-29.  
 XX  
 SQ Sequence 3 AA;  
 Query Match 75.0%; Score 9; DB 14; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 C 3  
 Db 2 c 2  
 RESULT 5  
 R34023  
 ID R34023 standard; peptide; 3 AA.  
 XX  
 AC R34023;  
 XX  
 XX 19-MAY-1993 (first entry)  
 DT  
 XX Metal trapping peptide intermediate.  
 DE  
 XX Electrostatic interaction; metalloprotein; binding site;  
 KW protecting group.  
 XX Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "HCl.H-Val"  
 FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH

FT Modified-site 3 of cysteine"  
 FT /note= "OME protected"  
 XX  
 PN JP04346999-A.  
 XX  
 XX 02-DEC-1992.  
 PD  
 XX 24-MAY-1991; 91JP-0120196.  
 PF  
 XX 24-MAY-1991; 91JP-0120196.  
 PR  
 XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.  
 PA  
 XX WPI; 1993-021449/03.  
 DR  
 XX New acyclic peptide with metal trapping activity - exhibits in  
 PT vivo metal transporting action and can be used as drug,  
 PT diagnostic agent or functional material  
 XX  
 PS Claim 3; Page 2; 9pp; Japanese.  
 CC The acyclic peptide (see R31340) with metal trapping activity may be  
 CC produced by fragment condensation using the peptide fragments given in  
 CC R34022-29.  
 XX  
 SQ Sequence 3 AA;  
 Query Match 75.0%; Score 9; DB 14; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 C 3  
 Db 2 c 2  
 RESULT 6  
 R51439  
 ID R51439 standard; peptide; 3 AA.  
 XX  
 AC R51439;  
 XX  
 XX 27-OCT-1994 (first entry)  
 DT  
 XX IGF-1 analogue N-terminal.  
 DE  
 XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;  
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9406445-A.  
 PN  
 XX 31-MAR-1994.  
 PD  
 XX 02-SEP-1993; 93WO-US08279.  
 PF  
 XX 17-SEP-1992; 92US-0947035.  
 PR  
 XX (EMBR-) EMBREX INC.  
 PA (GROP-) GROPEP PTY LTD.  
 PA (USDA) US SEC OF AGRIC.  
 XX  
 XX Ballard FJ, Francis GL, McMurtry JP, Phelps PV;  
 PI Walton PE;  
 XX  
 XX WPI; 1994-118144/14.  
 DR  
 XX Increasing growth of birds - with insulin-like growth factor  
 PT delivered to the egg before hatching esp. for increasing wt. gain  
 PT in chickens.

XX Claim 6; Page 37; 45pp; English.  
 XX Growth of birds is increased by (a) admin. to the bird, in ovo,  
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;  
 CC (b) incubating to hatch and (c) growing the birds for at least 3  
 CC weeks after hatch.  
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or  
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,  
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced  
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal  
 CC given in R51439-49.  
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced  
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent  
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.  
 CC comprises the N-terminal given in R51450-53.  
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human  
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid  
 CC N-terminal extension.  
 XX Sequence 3 AA;  
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
 |  
 Db 3 C 3

RESULT 7  
 R51440  
 ID R51440 standard; peptide; 3 AA.  
 XX R51440;  
 AC  
 XX  
 DT 27-OCT-1994 (first entry)  
 DE IGF-1 analogue N-terminal.  
 XX  
 XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;  
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09406445-A.  
 XX  
 PD 31-MAR-1994.  
 XX  
 PF 02-SEP-1993; 93WO-US08279.  
 XX  
 PR 17-SEP-1992; 92US-0947035.  
 XX  
 XX (EMBR-) EMBREX INC.  
 PA (GROP-) GROPEP PTY LTD.  
 PA (USDA) US SEC OF AGRIC.  
 XX  
 PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;  
 PI Walton PE;  
 XX  
 DR WPI; 1994-118144/14.  
 XX  
 XX Increasing growth of birds - with insulin-like growth factor  
 PT delivered to the egg before hatching esp. for increasing wt. gain  
 PT in chickens.  
 XX  
 XX Claim 6; Page 37; 45pp; English.  
 PS  
 XX Growth of birds is increased by (a) admin. to the bird, in ovo,  
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;  
 CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.  
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or  
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,  
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced  
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal  
 CC given in R51439-49.  
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced  
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent  
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.  
 CC comprises the N-terminal given in R51450-53.  
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human  
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid  
 CC N-terminal extension.  
 XX Sequence 3 AA;  
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
 |  
 Db 3 C 3

RESULT 8  
 R51441  
 ID R51441 standard; peptide; 3 AA.  
 XX R51441;  
 AC  
 XX  
 DT 27-OCT-1994 (first entry)  
 DE IGF-1 analogue N-terminal.  
 XX  
 XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;  
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09406445-A.  
 XX  
 PD 31-MAR-1994.  
 XX  
 PF 02-SEP-1993; 93WO-US08279.  
 XX  
 PR 17-SEP-1992; 92US-0947035.  
 XX  
 XX (EMBR-) EMBREX INC.  
 PA (GROP-) GROPEP PTY LTD.  
 PA (USDA) US SEC OF AGRIC.  
 XX  
 PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;  
 PI Walton PE;  
 XX  
 DR WPI; 1994-118144/14.  
 XX  
 XX Increasing growth of birds - with insulin-like growth factor  
 PT delivered to the egg before hatching esp. for increasing wt. gain  
 PT in chickens.  
 XX  
 XX Claim 6; Page 37; 45pp; English.  
 PS  
 XX Growth of birds is increased by (a) admin. to the bird, in ovo,  
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;  
 CC (b) incubating to hatch and (c) growing the birds for at least 3  
 CC weeks after hatch.  
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or  
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,  
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced  
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal  
 CC given in R51439-49.



## RESULT 11

W56211  
ID W56211 standard; peptide; 3 AA.  
XX AC W56211;  
XX DT 20-JUL-1998 (first entry)  
XX DE Anti-inflammatory tripeptide.  
XX DE Anti-inflammatory tripeptide.  
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;  
KW T-cell inhibitory activity; adherence; extracellular matrix;  
KW up-regulation; fas receptor expression; inflammation.  
XX OS Synthetic.

XX WO9809985-A2.  
XX PN 12-MAR-1998.  
XX PD 03-SEP-1997; 97WO-IL00295.  
XX PF 28-MAY-1997; 97US-0864301.  
XX PR 03-SEP-1996; 96US-0025376.  
XX PR 20-NOV-1996; 96US-0753141.

XX (YEDA ) YEDA RES & DEV CO LTD.  
XX PA Beserman P, Eisenbachschwartz M, Hirschberg DL;  
XX PI WPI; 1998-193550/17.  
XX DR

XX Anti-inflammatory peptides and derivatives - used for treating, e.g.  
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,  
PT shock, HIV infection, transplant rejection or Alzheimer's disease  
XX Claim 6; Page 35; 42pp; English.  
XX W56171-248 represent anti-inflammatory tripeptides of the invention.  
CC They are derived from the formulae:  
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where  
CC Xaa = any amino acid residue.  
CC Cyclic derivatives of the peptides also function as anti-inflammatory  
CC agents. The peptides can be covalently linked to one another either  
CC directly or through a spacer. The peptides and their derivatives have  
CC macrophage inhibitory and T-cell inhibitory activity and thus,  
CC anti-inflammatory activity. The peptides and compositions have  
CC anti-immune activity, i.e. inhibitory effects against a cellular and  
CC humoral immune response, including a response not associated with  
CC inflammation. The peptides also inhibit the ability of macrophages and  
CC T-cells to adhere to extracellular matrix components and fibronectin, as  
CC well as up-regulated fas receptor expression in T-cells. They can be used  
CC to inhibit unwanted immune reaction and inflammation.  
XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
DB 1 C 1

## RESULT 12

W56200  
ID W56200 standard; peptide; 3 AA.  
XX AC W56200;  
XX DT 20-JUL-1998 (first entry)

XX DE

XX Anti-inflammatory tripeptide.

XX Anti-inflammatory; macrophage inhibitory activity; fibronectin;  
KW T-cell inhibitory activity; adherence; extracellular matrix;  
KW up-regulation; fas receptor expression; inflammation.  
XX OS Synthetic.

XX WO9809985-A2.  
XX PN 12-MAR-1998.  
XX PD 03-SEP-1997; 97WO-IL00295.  
XX PF 28-MAY-1997; 97US-0864301.  
XX PR 03-SEP-1996; 96US-0025376.  
XX PR 20-NOV-1996; 96US-0753141.

XX (YEDA ) YEDA RES & DEV CO LTD.  
XX PA Beserman P, Eisenbachschwartz M, Hirschberg DL;  
XX PI WPI; 1998-193550/17.  
XX DR

XX Anti-inflammatory peptides and derivatives - used for treating, e.g.  
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,  
PT shock, HIV infection, transplant rejection or Alzheimer's disease  
XX Claim 5; Page 34; 42pp; English.  
XX W56171-248 represent anti-inflammatory tripeptides of the invention.  
CC They are derived from the formulae:  
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where  
CC Xaa = any amino acid residue.  
CC Cyclic derivatives of the peptides also function as anti-inflammatory  
CC agents. The peptides can be covalently linked to one another either  
CC directly or through a spacer. The peptides and their derivatives have  
CC macrophage inhibitory and T-cell inhibitory activity and thus,  
CC anti-inflammatory activity. The peptides and compositions have  
CC anti-immune activity, i.e. inhibitory effects against a cellular and  
CC humoral immune response, including a response not associated with  
CC inflammation. The peptides also inhibit the ability of macrophages and  
CC T-cells to adhere to extracellular matrix components and fibronectin, as  
CC well as up-regulated fas receptor expression in T-cells. They can be used  
CC to inhibit unwanted immune reaction and inflammation.  
XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
DB 3 C 3

## RESULT 13

W56172  
ID W56172 standard; peptide; 3 AA.  
XX AC W56172;  
XX DT 20-JUL-1998 (first entry)  
XX DE Anti-inflammatory tripeptide.  
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;  
KW T-cell inhibitory activity; adherence; extracellular matrix;  
KW up-regulation; fas receptor expression; inflammation.  
XX

OS Synthetic.  
 PN WO9809985-A2.  
 XX  
 PD 12-MAR-1998.  
 XX  
 PF 03-SEP-1997; 97WO-IL00295.  
 XX  
 PR 28-MAY-1997; 97US-0864301.  
 PR 03-SEP-1996; 96US-0025376.  
 PR 20-NOV-1996; 96US-0753141.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Beserman P, Eisenbachschwartz M, Hirschberg DL;  
 XX  
 DR WPI; 1998-193550/17.  
 XX  
 PT Anti-inflammatory peptides and derivatives - used for treating, e.g.  
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,  
 PT shock, HIV infection, transplant rejection or Alzheimer's disease  
 XX  
 PS Claim 3; Page 34; 42pp; English.  
 XX  
 CC W56171-248 represent anti-inflammatory tripeptides of the invention.  
 CC They are derived from the formulae:  
 CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where  
 CC Xaa = any amino acid residue.  
 CC Cyclic derivatives of the peptides also function as anti-inflammatory  
 CC agents. The peptides can be covalently linked to one another either  
 CC directly or through a spacer. The peptides and their derivatives have  
 CC macrophage inhibitory and T-cell inhibitory activity and thus,  
 CC anti-inflammatory activity. The peptides and compositions have  
 CC anti-immune activity, i.e. inhibitory effects against a cellular and  
 CC humoral immune response, including a response not associated with  
 CC inflammation. The peptides also inhibit the ability of macrophages and  
 CC T-cells to adhere to extracellular matrix components and fibronectin, as  
 CC well as up-regulated fas receptor expression in T-cells. They can be used  
 CC to inhibit unwanted immune reaction and inflammation.  
 XX  
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 C 3  
 Db 1 c 1

RESULT 14  
 W88037  
 ID W88037 standard; peptide; 3 AA.  
 AC W88037;  
 XX  
 DT 09-APR-1999 (first entry)  
 DE  
 XX Peptide used in the hair composition of the invention.  
 XX Hair; styling; wave.  
 XX  
 OS Synthetic.  
 XX  
 PN JP11012138-A.  
 XX  
 PD 19-JAN-1999.  
 XX  
 PF 18-JUN-1997; 97JP-0161657.  
 XX

PR 18-JUN-1997; 97JP-0161657.  
 XX  
 PA (LIOY ) LION CORP.  
 XX  
 DR WPI; 1999-148442/13.  
 XX  
 PT New composition for hair - comprises oligopeptide having more than 2  
 PT cysteine residues and reducing agent  
 XX  
 PS Example 2; Page 6; 17pp; Japanese.  
 XX  
 CC Peptides W88033-39 are used in the hair composition of the invention.  
 CC The specification describes a hair composition that comprises at  
 CC least one oligopeptide having more than two cysteine residues and more  
 CC than three amino acid residues of the same kind (except cysteine) and a  
 CC reducing agent. The composition is useful for styling hair to take  
 CC various shapes and waves safely and effectively.  
 XX  
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 20; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 C 3  
 Db 1 c 1

RESULT 15  
 Y51896  
 ID Y51896 standard; peptide; 3 AA.  
 AC Y51896;  
 XX  
 DT 16-JUN-2000 (first entry)  
 DE  
 XX Biostatin TT232 synthesising peptide 1.  
 KW Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor;  
 KW cellular proliferation inhibition; somatostatin; antitumor.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "TFA\*Lys(2)"  
 FT Modified-site 2 /note= "Cys(Acm)"  
 FT Modified-site 3 /note= "Thr(tBu) with C-terminal amide group"  
 FT  
 XX WO200011032-A2.  
 PN  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-EP06131.  
 XX  
 PR 20-AUG-1998; 98WO-EP05306.  
 XX  
 PA (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.  
 XX  
 PI Braun G, Lifferth A, Birr C;  
 XX  
 DR WPI; 2000-224663/19.  
 XX  
 PT Biostatin preparation in high yield by solid synthesis, including  
 PT closure of disulfide bridge before cleavage from support, useful as  
 PT antitumor agent -  
 XX  
 PS Example 4; Page 23; 33pp; German.  
 XX



CC This invention describes a novel method for the solid phase (SP)  
CC synthesis of biostatin (TT 232) (I) which includes closing the disulfide  
CC bridge by oxidation of the completely or partially constructed peptide  
CC while still bonded to the solid phase. The products of the invention have  
CC cytostatic activity and are tyrosine kinase inhibitors. (I) inhibits the  
CC tyrosine kinase activity of various human stomach cancer cell lines and  
CC thus inhibits cellular proliferation. The heptapeptide (I) described in  
CC the invention is a somatostatin analog which shows strong antitumor  
CC activity in vitro and in vivo. The SP synthesis method gives (I) is more  
CC easily and in markedly higher yield than by the method of EP505680, in  
CC which the cyclization is carried out after cleaving the peptide from the  
CC resin. The solution method is also a simple synthesis of (I) in high  
CC yield; typically the tert-butyl-protected precursor can be oxidized in  
CC a yield of 70-80%. Y51896-Y51900 represent peptides used in the  
CC synthesis of biostatin TT232 described in the method of the invention.  
XX  
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 21; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 2 c 2

Search completed: February 5, 2001, 12:01:19  
Job time: 366 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:53 ; Search time 30.91 Seconds  
(without alignments)  
2.324 Million cell updates/sec

Title: US-09-687-267-5

Perfect score: 12

Sequence: 1 XXCX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_patents\_AA.\*

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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/PCTRUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	75.0	2	1	US-07-791-213D-23
2	9	75.0	2	1	US-07-791-213D-39
3	9	75.0	2	1	US-08-133-804-9
4	9	75.0	2	1	US-08-354-240A-12
5	9	75.0	2	1	US-08-461-838-9
6	9	75.0	2	1	US-08-293-150A-23
7	9	75.0	2	1	US-08-293-150A-39
8	9	75.0	2	2	US-08-461-386-9
9	9	75.0	2	2	US-08-465-380-307
10	9	75.0	2	2	US-08-486-397-307
11	9	75.0	2	2	US-08-486-399-307
12	9	75.0	2	2	US-08-461-965-307
13	9	75.0	2	2	US-08-634-641-307
14	9	75.0	2	2	US-08-818-253-52
15	9	75.0	2	3	US-09-249-471-307
16	9	75.0	2	3	US-09-249-472-307
17	9	75.0	2	3	US-09-249-451-307
18	9	75.0	2	3	US-08-809-455-307
19	9	75.0	2	3	US-09-249-461-307
20	9	75.0	2	3	US-09-249-448-307
21	9	75.0	3	1	US-07-791-213D-22
22	9	75.0	3	1	US-07-791-213D-38
23	9	75.0	3	1	US-07-945-982-2
24	9	75.0	3	1	US-07-945-982-8
25	9	75.0	3	1	US-07-947-035-3
26	9	75.0	3	1	US-07-947-035-4
27	9	75.0	3	1	US-07-947-035-5
28	9	75.0	3	1	US-08-285-443-4

29 9 75.0 3 1 US-08-079-812-31 Sequence 31, Appl  
30 9 75.0 3 1 US-08-122-510-11 Sequence 11, Appl  
31 9 75.0 3 1 US-08-122-510-12 Sequence 12, Appl  
32 9 75.0 3 1 US-08-122-510-13 Sequence 13, Appl  
33 9 75.0 3 1 US-07-789-913-26 Sequence 26, Appl  
34 9 75.0 3 1 US-08-371-930-4 Sequence 4, Appl  
35 9 75.0 3 1 US-08-049-794-26 Sequence 26, Appl  
36 9 75.0 3 1 US-08-372-453-2 Sequence 2, Appl  
37 9 75.0 3 1 US-08-372-455-8 Sequence 8, Appl  
38 9 75.0 3 1 US-08-321-585A-1 Sequence 1, Appl  
39 9 75.0 3 1 US-08-321-585A-2 Sequence 2, Appl  
40 9 75.0 3 1 US-08-321-585A-3 Sequence 3, Appl  
41 9 75.0 3 1 US-08-446-908-14 Sequence 14, Appl  
42 9 75.0 3 1 US-08-231-205A-14 Sequence 14, Appl  
43 9 75.0 3 1 US-08-293-150A-22 Sequence 22, Appl  
44 9 75.0 3 1 US-08-293-150A-38 Sequence 38, Appl  
45 9 75.0 3 3 US-08-447-515-12 Sequence 12, Appl

#### ALIGNMENTS

##### RESULT 1

US-07-791-213D-23  
; Sequence 23, Application US/07791213D  
; Patent No. 5409895  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07791,213D  
; FILING DATE: 13-NOV-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-791-213D-23

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 2 C 2

RESULT 2  
US-07-791-213D-39  
; Sequence 39, Application US/07791213D  
; Patent No. 5409895  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOSUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791,213D  
; FILING DATE: 13-NOV-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-791-213D-39

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 1 C 1

RESULT 3  
US-08-133-804-9  
; Sequence 9, Application US/08133804  
; Patent No. 5534254  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For

ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 34506.029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-831-2100  
TELEFAX: 608-831-2106  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-354-240A-12

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 1 C 1

RESULT 5  
US-08-461-838-9  
Sequence 9, Application US/08461838  
Patent No. 5753204  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
NUMBER OF INVENTION: Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,838  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..2  
OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"  
US-08-461-838-9

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 C 3  
|  
Db 2 C 2

## RESULT 6

US-08-293-150A-23  
Sequence 23, Application US/08293150A  
Patent No. 5792629  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NORUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TREATING USING THE SAME  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-5620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-293-150A-23

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 2 C 2

RESULT 7  
US-08-293-150A-39  
Sequence 39, Application US/08293150A

Patent No. 5792629  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshihiko  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TITLE OF INVENTION: TREATING USING THE SAME  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-293-150A-39

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
Db 1 C 1

RESULT 8  
US-08-461-386-9  
Sequence 9, Application US/08461386  
Patent No. 5837846  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
TITLE OF INVENTION: Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston

STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,386  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..2  
OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"  
US-08-461-386-9

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
Db 2 C 2

RESULT 9  
US-08-465-380-307  
Sequence 307, Application US/08465380  
Patent No. 5863894  
GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Menssens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,380  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/268  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.  
US-08-465-380-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 1 C 1

RESULT 10  
US-08-486-397-307  
; Sequence 307, Application US/08486397  
; Patent No. 5866542  
; GENERAL INFORMATION:  
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
; APPLICANT: Peter W. Bergum  
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
; NUMBER OF SEQUENCES: 357  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,397  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 213/269  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440

;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.  
US-08-486-397-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 1 C 1

RESULT 11  
US-08-486-399-307  
; Sequence 307, Application US/08486399  
; Patent No. 5866543  
; GENERAL INFORMATION:  
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
; APPLICANT: Peter W. Bergum  
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,399  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 213/270  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; amino acid.

US-08-486-399-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 1 C 1

RESULT 12

US-08-461-965-307  
; Sequence 307, Application US/08461965  
; Patent No. 5872098  
; GENERAL INFORMATION:  
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
; APPLICANT: Peter W. Bergum  
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,965  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 210/243  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; amino acid.  
US-08-461-965-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 1 C 1

RESULT 13

US-08-634-641-307  
; Sequence 307, Application US/08634641  
; Patent No. 5955294  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George P. Vlasuk  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Mensens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Gansemans, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew  
; APPLICANT: Bergum, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/634,641  
; FILING DATE: April 19, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13231  
; FILING DATE: October 17, 1995  
; APPLICATION NUMBER: 08/486,399  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/486,397  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/465,380  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/461,965  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 219/136  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; amino acid.  
US-08-634-641-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
Db 1 C 1

## RESULT 14

US-08-818-253-52  
; Sequence 52, Application US/08818253  
; Patent No. 5998204  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Miyawaki, Atsushi  
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
; TITLE OF INVENTION: DETECTION OF ANALYTES  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,253  
; FILING DATE: 14-MAR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Ph.D., Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07257/043001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-818-253-52

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
Db 1 C 1

## RESULT 15

US-09-249-471-307  
; Sequence 307, Application US/09249471  
; Patent No. 604041  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George Phillip  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Messens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Gansemans, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew  
; APPLICANT: Bergum, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/249,471  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/809,455  
; FILING DATE: April 17, 1997  
; APPLICATION NUMBER: PCT/US95/13231  
; FILING DATE: October 17, 1995  
; APPLICATION NUMBER: 08/486,399  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/486,397  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/465,380  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/461,965  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 216/270  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; OTHER INFORMATION: amino acid.  
US-09-249-471-307

Query Match 75.0%; Score 9; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
Db 1 C 1

Search completed: February 5, 2001, 12:01:54  
Job time: 336 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:02:32 ; Search time 34.92 Seconds  
(without alignments)  
7.778 Million cell updates/sec

Title: US-09-687-267-5

Perfect score: 12

Sequence: 1 XXCX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_66:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	75.0	3	2 A22565	R-phycoerythrin al
2	9	75.0	4	2 I51049	metallothionein-A
3	9	75.0	4	2 S43959	Ig mu chain V regi
4	9	75.0	4	2 S52338	pallidipin - assas
5	9	75.0	5	2 B22565	R-phycoerythrin al
6	9	75.0	5	2 F22565	R-phycoerythrin ga
7	9	75.0	5	2 A33882	cadmium-binding pe
8	9	75.0	5	2 B45525	actin I - malaria
9	9	75.0	5	2 S65726	hemoglobin, extrac
10	9	75.0	6	2 J00355	lipopeptide WS1279
11	9	75.0	6	2 C22565	R-phycoerythrin be
12	9	75.0	6	2 I37027	protamine p1 - gor
13	9	75.0	6	2 I37263	Y protein - human
14	9	75.0	6	2 S29881	Na+/K+-exchanging
15	9	75.0	6	2 H48394	glycoprotein compo
16	9	75.0	6	2 I67345	MHC H2-K-k cell su
17	9	75.0	6	2 I65546	MHC H2-L antigen -
18	9	75.0	6	2 P70652	T-cell receptor be
19	9	75.0	6	2 F41946	laminin B1 - weste
20	9	75.0	6	2 I49421	hypothetical TGL3
21	9	75.0	6	4 I79564	Ig heavy chain V r
22	9	75.0	7	2 PH1408	venom heptapeptide
23	9	75.0	7	2 A58512	hypothetical prote
24	9	75.0	7	2 S08606	mablinin II chain
25	9	75.0	7	2 S38516	vicillin 57K chain
26	9	75.0	7	2 B34818	cadmium-binding he
27	9	75.0	7	2 B33882	acetylcholinestera
28	9	75.0	7	2 A34026	formylglycinamide
29	9	75.0	7	2 A12016	

30 9 75.0 7 2 PH1602 Ig H chain V-D-J r

31 9 75.0 7 2 PH0932 T-cell receptor be

32 9 75.0 7 4 I56695 hypothetical I2 pr

33 9 75.0 8 2 PH1407 Ig heavy chain V r

34 9 75.0 8 2 S59622 metallothionein is

35 9 75.0 8 2 XGHUEU urine glycopeptide

36 9 75.0 8 2 A25836 L-serine dehydrata

37 9 75.0 8 2 PCI002 leucine--trna liga

38 9 75.0 8 2 S19288 acylase - Kluyvera

39 9 75.0 8 2 A37521 R-phycoerythrin ga

40 9 75.0 8 2 C61512 variant surface gl

41 9 75.0 8 2 D61512 variant surface gl

42 9 75.0 8 2 PH1618 Ig H chain V-D-J r

43 9 75.0 8 2 PH0803 T-cell receptor al

44 9 75.0 8 2 I57018 gene Cfr protein

45 9 75.0 8 2 PH0934 T-cell receptor be

#### ALIGNMENTS

##### RESULT 1

A22565 R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)

C:Species: Gastroclonium coulteri

C>Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993

C:Accession: A22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: A22565

A:Molecule type: protein

A:Residues: 1-3 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
Db 1 C 1

##### RESULT 2

I51049 metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: I51049

R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)

A:Reference number: I51049; MUID:95324545

A:Accession: I51049

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <OLS>

A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 75.0%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
Db 4 C 4

##### RESULT 3

S43959

Ig mu chain V region (clone 13) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
C:Accession: S43959  
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;  
Nucleic Acids Res. 22, 1389-1393, 1994  
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
A:Reference number: S43956; MUID:94248036  
A:Accession: S43959  
A:Molecule type: DNA  
A:Residues: 1-4 <WAG>  
C:Keywords: immunoglobulin

Query Match 75.0%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3

Db 2 C 2

RESULT 4

S55238

pallidipin - assassin bug (fragment)

C:Species: Triatoma pallidipennis (assassin bug)

C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000

C:Accession: S55238

R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleuning

Biochem. J. 307, 465-470, 1995

A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib

A:Reference number: S55238; MUID:95251610

A:Accession: S55238

A:Molecule type: protein

A:Residues: 1-4 <HAE>

Query Match 75.0%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3

Db 3 C 3

RESULT 5

B22565

R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)

C:Species: Gastroclonium coulteri

C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993

C:Accession: B22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: B22565

A:Molecule type: protein

A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3

Db 2 C 2

RESULT 6

F22565

R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)  
C:Species: Gastroclonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: F22565  
R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: F22565

A:Molecule type: protein

A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3

Db 3 C 3

RESULT 7

A33882

cadmium-binding pentapeptide - downy thornapple

C:Species: Datura innoxia (downy thornapple)

C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 18-Jun-1993

C:Accession: A33882

R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987

A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plan

A:Reference number: A94182; MUID:88016144

A:Accession: A33882

A:Molecule type: protein

A:Residues: 1-5 <JAC>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3

Db 2 C 2

RESULT 8

B45525

actin I - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C:Date: 03-Jun-1993 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000

C:Accession: B45525

R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoen

Mol. Biochem. Parasitol. 35, 167-176, 1989

A:Title: Stage-specific expression and genomic organization of the actin genes of the

A:Reference number: A45525; MUID:89364996

A:Accession: B45525

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <WES>

A:Cross-references: GB:J03988

A>Note: the authors translated the codon GAA for residue 3 as Gly

C:Comment: The actin I gene contains no introns.

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3

Db 4 C 4

RESULT 9  
S65726  
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)  
C:Species: Lumbricus terrestris (common earthworm)  
C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65726  
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.  
Biochim. Biophys. Acta 1292, 273-280, 1996  
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A:Reference number: S65721; MUID:96176855  
A:Accession: S65726  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <FUS>

Query Match 75.0%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
DB 4 C 4

RESULT 10  
JU0355  
lipopeptide WS1279 [validated] - Streptomyces willmorei  
C:Species: Streptomyces willmorei  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: JU0355  
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.  
Chem. Pharm. Bull. 39, 607-611, 1991  
A:Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin  
A:Reference number: JU0355; MUID:91300586  
A:Accession: JU0355  
A:Molecule type: protein  
A:Residues: 1-6 <TSU>  
A:Note: the structure was confirmed by synthesis  
C:Keywords: blocked amino end; lipoprotein  
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental  
F:1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
DB 1 C 1

RESULT 11  
C22565  
R-phycoerythrin beta-1 chain - red alga (Gastrocloonium coulteri) (fragment)  
C:Species: Gastrocloonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: C22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601  
A:Accession: C22565  
A:Molecule type: protein  
A:Residues: 1-6 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
DB 1 C 1

RESULT 12  
I37027  
protamine P1 - gorilla (fragment)  
C:Species: Gorilla gorilla (gorilla)  
C:Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jul-2000  
C:Accession: I37027  
R:Queralt, R.; Oliva, R.  
Gene 133, 197-204, 1993  
A:Title: Identification of conserved potential regulatory sequences of the protamine  
A:Reference number: I37013; MUID:94040810  
A:Accession: I37027  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
DB 6 C 6

RESULT 13  
I37263  
Y protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I37263  
R:Waeber, G.; Habener, J.F.  
Endocrinology 131, 2010-2015, 1992  
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative  
A:Reference number: I37263; MUID:93010691  
A:Accession: I37263  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816  
C:Genetics:  
A:Gene: CREB

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
DB 4 C 4

RESULT 14  
S29881  
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 07-May-1999  
C:Accession: S29881  
R:Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.  
J. Biol. Chem. 260, 3852-3859, 1985  
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases arou  
A:Reference number: S29881; MUID:85131201  
A:Accession: S29881  
A:Molecule type: protein  
A:Residues: 1-6 <WAL>  
A:Experimental source: kidney

C;keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;  
F;4/Active site: Asp (aspartylphosphate intermediate) #status Predicted

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 2 C 2

## RESULT 15

H48394  
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C;Accession: H48394  
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
II-like sequences.  
A;Reference number: A48394; MUID:93250576  
A;Accession: H48394  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <MAT>  
A;Experimental source: milk  
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)  
C;keywords: glycoprotein

Query Match 75.0%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
|  
Db 6 C 6

Search completed: February 5, 2001, 12:02:32  
Job time: 289 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2001, 12:06:02 ; Search time 20.72 Seconds  
(without alignments)  
6.234 Million cell updates/sec

Title: US-09-687-267-5  
Perfect score: 12  
Sequence: 1 XXCX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues  
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	9	75.0	8 1 ACT_CARMA	P80709 carcinus ma
2	9	75.0	8 1 GLUR_HUMAN	P02729 homo sapien
3	9	75.0	9 1 CCAP_CARMA	P38556 carcinus ma
4	9	75.0	9 1 CONO_CONGE	P05486 conus geogr
5	9	75.0	9 1 CONO_CONST	P05487 conus stria
6	9	75.0	9 1 DNF1_LOCOMI	P16339 locusta mig
7	9	75.0	9 1 ISOT_CYPCA	P42993 cyprinus ca
8	9	75.0	9 1 MGMT_BOVIN	P29177 bos taurus
9	9	75.0	9 1 OXYA_SCYCA	P42996 scyllorhinu
10	9	75.0	9 1 OXYA_SQUAC	P42999 squallus aca
11	9	75.0	9 1 OXYF_SCYCA	P42997 scyllorhinu
12	9	75.0	9 1 OXYT_BUFRE	P42995 bufo regula
13	9	75.0	9 1 OXYT_CYPCA	P23879 cyprinus ca
14	9	75.0	9 1 OXYT_EISFO	P42998 eisenia foe
15	9	75.0	9 1 OXYT_OCTVU	P80027 octopus vul
16	9	75.0	9 1 OXYT_RABIT	P32878 oryctolagus
17	9	75.0	9 1 OXYT_RAJCL	P42994 raja clavac
18	9	75.0	9 1 OXYV_SQUAC	P43000 squallus aca
19	9	75.0	9 1 RS11_SALTY	O54296 salmonella
20	9	75.0	9 1 SAP_STOVA	P24047 stomopneute
21	9	75.0	9 1 TAL1_PICJA	P17440 pichia jadi
22	9	75.0	9 1 TAL3_PICJA	P17441 pichia jadi
23	9	75.0	10 1 GLEM_HUMAN	P02728 homo sapien
24	9	75.0	10 1 GON2_CHEPR	P80678 chelyosoma
25	9	75.0	10 1 RCA_FINPS	P81084 pinus pinas
26	9	75.0	12 1 CXA1_CONIM	P50983 conus imper
27	9	75.0	12 1 NO40_LOTJA	O22426 lotus japon
28	9	75.0	12 1 NO40_SESRO	O24369 sesbania ro
29	9	75.0	12 1 NO40_SOYBN	P55960 glycine max
30	9	75.0	12 1 R16_GINBI	P36207 ginkgo bilo
31	9	75.0	12 1 TAL0_TREME	P01371 tremella me
32	9	75.0	12 1 UR2A_CATCO	P04558 catostomus
33	9	75.0	12 1 UR2B_CATCO	P04559 catostomus

34 9 75.0 12 1 UR2B\_CYPCA P04561 cyprinus ca  
35 9 75.0 12 1 UR2\_GILMI P01147 gillichthys  
36 9 75.0 12 1 UR2\_POLSP P81022 polyodon sp  
37 9 75.0 12 1 UR2\_SCYCA P35490 scyllorhinu  
38 9 75.0 12 1 YZPY\_ECOLI P17776 escherichia  
39 9 75.0 13 1 ACT7\_SOYBN P15987 glycine max  
40 9 75.0 13 1 CXAL\_CONST P15471 conus stria  
41 9 75.0 13 1 CXA2\_CONGE P01520 conus geogr  
42 9 75.0 13 1 CXAA\_CONST P28878 conus stria  
43 9 75.0 13 1 CXET\_CONTE P81755 conus texti  
44 9 75.0 13 1 GER1\_HORVU P28525 hordeum vul  
45 9 75.0 13 1 GER2\_HORVU P28526 hordeum vul

#### ALIGNMENTS

RESULT 1  
ACT\_CARMA  
ID ACT\_CARMA STANDARD; PRT; 8 AA.  
AC P80709;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ACTIN (FRAGMENT).  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
RN [1]  
RP SEQUENCE.  
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
RA Baghdassarian D.; An enzyme implicated in crab steroidogenesis.;  
RT "A transalcolase. An enzyme implicated in crab steroidogenesis.";  
RL Endocrine 5:23-32(1996).  
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED  
CC IN ALL EUKARYOTIC CELLS.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
CC 6.8, ITS MW IS: 46 KDA.  
CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.  
DR INTERPRO; IPR000279; .  
DR PROSITE; PS00406; ACTINS\_1; PARTIAL.  
DR PROSITE; PS00432; ACTINS\_2; PARTIAL.  
DR PROSITE; PS01132; ACTINS\_ACT\_LIKE; PARTIAL.  
KW Structural protein.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
Db 2 C 2

RESULT 2  
GLUR\_HUMAN  
ID GLUR\_HUMAN STANDARD; PRT; 8 AA.  
AC P02729;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE URINE GLYCOPETIDE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]

RP SEQUENCE  
RX MEDLINE=72062338; PubMed=5126885;  
RA Lote C.J., Weiss J.B.;  
RT "Identification in urine of a low-molecular-weight highly polar  
RT glycopeptide containing cysteinyl-galactose.";  
RL Biochem J. 123:25p-25p(1971).  
CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE  
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN  
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A  
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.  
DR PIR: A03188; XGHUEV.  
KW Glycoprotein.  
FT CARBOHYD  
SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5B1E1E CRC64;  
  
Query Match 75.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 C 3  
DB 1 C 1  
  
RESULT 3  
CCAP\_CARMA STANDARD; PRT; 9 AA.  
ID CCAP\_CARMA  
AC P38556;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CARDIOACTIVE PEPTIDE (CCAP).  
OS Carcinus maenas (Common shore crab) (Green crab),  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),  
OS Tenebrio molitor (Yellow mealworm), and  
OS Spodoptera eridania (Southern armyworm).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C. MAENAS; TISSUE=PERICARDIAL ORGANS;  
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;  
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
RT shore crab Carcinus maenas.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=M. SEXTA;  
RX MEDLINE=93050243; PubMed=1426284;  
RA Cheung C.C., Loi P.K., Sylvester A.W., Lee T.D., Tublitz N.J.;  
RT "Primary structure of a cardioactive neuropeptide from the tobacco  
RT hawkmoth, Manduca sexta.";  
RL FEBS Lett. 313:165-168(1992).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=T. MOLITOR, AND S. ERIDANIA; TISSUE=HEAD;  
RX MEDLINE=94176032; PubMed=8129851;  
RA Furuoya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,  
RA Schooley D.A.;  
RT "Isolation and identification of a cardioactive peptide from Tenebrio  
RT molitor and Spodoptera eridania.";  
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).  
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.  
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
CC INTO THE HEMOLYPH.  
DR PIR: A26363; A26363.  
DR PIR: S27233; S27233.  
KW Neuropeptide; Amidation.  
FT DISULFID 3 9  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 C 3  
DB 1 C 1  
  
RESULT 4  
CONO\_CONGE STANDARD; PRT; 9 AA.  
ID CONO\_CONGE  
AC P05486;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE LYS-CONOPRESSIN G.  
OS Conus geographus (Geography cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88058932; PubMed=3680228;  
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
RA Gray W.R., Olivera B.M.;  
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of  
RT peptides from Conus geographus and Conus straitus venoms.";  
RL J. Biol. Chem. 262:15821-15824(1987).  
RN [2]  
RP REVIEW.  
RX MEDLINE=89024586; PubMed=3052286;  
RA Gray W.R., Olivera B.M., Cruz L.J.;  
RT "Peptide toxins from venomous Conus snails.";  
RL Annu. Rev. Biochem. 57:665-700(1988).  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR: A28495; A28495.  
DR INTERPRO: IPR000981;  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1037 MW; D4FC276E84540059 CRC64;  
  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 C 3  
DB 1 C 1  
  
RESULT 5  
CONO\_CONST STANDARD; PRT; 9 AA.  
ID CONO\_CONST  
AC P05487;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ARG-CONOPRESSIN S.  
OS Conus striatus (Striated cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88058932; PubMed=3680228;  
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
RA Gray W.R., Olivera B.M.;  
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of

RT peptides from Conus geographus and Conus straitus venoms.";  
 RL J. Biol. Chem. 262:15821-15824(1987).  
 RN [2]

RP REVIEW.  
 RX MEDLINE=89024586; PubMed=3052286;  
 RA Gray W.R., Olivera B.M., Cruz L.J.;  
 RT "Peptide toxins from venomous Conus snails.";  
 RL Annu. Rev. Biochem. 57:665-700(1988).  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR; B28495; B28495.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
 |  
 Db 1 C 1

RESULT 6  
 DNFI\_LOCFMI STANDARD; PRT; 9 AA.  
 AC P16339;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE LOCUPRESSIN (DIURETIC NEUROPEPTIDE FI/F2).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;  
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=SUBESOPHAGEAL GANGLION, AND THORACIC GANGLION;  
 RX MEDLINE=88077077; PubMed=3689410;  
 RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,  
 RA Delaage M., Schooley D.A.;  
 RT "Identification of an arginine vasopressin-like diuretic hormone from  
 RT Locusta migratoria.";  
 RL Biochem. Biophys. Res. Commun. 149:180-186(1987).  
 CC -!- FUNCTION: DIURETIC HORMONE.  
 CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR PIR; A29477; A29477.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Neuropeptide; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
 |  
 Db 1 C 1

RESULT 7  
 ISOT\_CYPCA STANDARD; PRT; 9 AA.  
 AC P42993;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE ISOTOCIN.  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=PIUITARY;  
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
 RT "Characterization of neurohypophyseal hormones from a fresh water bony  
 RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea  
 RT water bony fish.";  
 RL Comp. Biochem. Physiol. 14:245-254(1965).  
 CC -!- FUNCTION: ANTIDIURETIC HORMONE.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR; A61364; A61364.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
 |  
 Db 1 C 1

RESULT 8  
 MGMT\_BOVIN STANDARD; PRT; 9 AA.  
 AC P29177;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) (FRAGMENT).  
 GN MGMT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=THYMUS;  
 RX MEDLINE=90174912; PubMed=2308822;  
 RA Rydberg B., Hall J., Karan P.;  
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA  
 RT methyltransferase.";  
 RL Nucleic Acids Res. 18:17-21(1990).  
 CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY  
 CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE  
 CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS  
 CC IRREVERSIBLY INACTIVATED  
 CC -!- CATALYTIC ACTIVITY: DNA (CONTAINING O6-METHYLGUANINE) + PROTEIN  
 CC L-CYSTEINE -> DNA (WITHOUT O6-METHYLGUANINE) + PROTEIN S-METHYL-  
 CC L-CYSTEINE.  
 CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OCT METHYLTRANSFERASE  
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.  
 DR INTERPRO: IPR001497; -.



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DR PROSITE; PS00374; MGMT: PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 9
OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY;
RA Chauvet J., Rouille Y., Chauvet C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
isolated from the spotted dogfish (Scyllorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT MOD_RES 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 10
OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN (ASPARTOCIN).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
RN [1]
RP SEQUENCE.
RX Acher R., Chauvet J., Chauvet M.-T.;

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RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
spiny dog-fish (Squalus acanthias).";
C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT MOD_RES 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 11
OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHASVATOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauvet C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
isolated from the spotted dogfish (Scyllorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -1- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT MOD_RES 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 12
OXYT_BUFRE

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ID OXYT\_BUFRE STANDARD; PRT; 9 AA.  
AC P42995;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE SERITOCIN.  
OS Bufo regularis (African toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;  
OC Bufo.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=PITUITARY NEUROINTERMEDIATE LOBE;  
RX MEDLINE=96059313; PubMed=7591488;  
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;  
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),  
RT identified in a dryness-resistant African toad, Bufo regularis.;  
RL Int. J. Pept. Protein Res. 45:482-487(1995).  
CC -!- FUNCTION: DEVOID OF OXYTOCIN ACTIVITY.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR INTERPRO: IPR000981; .  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
FT SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;  
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 C 3  
DB 1 C 1  
RESULT 13  
OXYT\_CYPCA  
ID OXYT\_CYPCA STANDARD; PRT; 9 AA.  
AC P23879;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE VASOTOCIN.  
OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C.CARPPIO; TISSUE=PITUITARY;  
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
RT "Characterization of neurohypophyseal hormones from a fresh water bony  
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea  
RT water bony fishs.;  
RL Comp. Biochem. Physiol. 14:245-254(1965).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=P.MARINUS; TISSUE=PITUITARY;  
RX MEDLINE=88225976; PubMed=3371648;  
RA Lane T.F., Sower S.A., Kawauchi H.;  
RT "Arginine vasotocin from the pituitary gland of the lamprey  
RT (Petromyzon marinus): isolation and amino acid sequence.;  
RL Gen. Comp. Endocrinol. 70:152-157(1988).  
CC -!- FUNCTION: ANTIDIURETIC HORMONE.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR; B61364; B61364.  
DR PIR; S06375; S06375.  
DR INTERPRO: IPR000981; .  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.

KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
FT SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;  
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 C 3  
DB 1 C 1  
RESULT 14  
OXYT\_EISFO  
ID OXYT\_EISFO STANDARD; PRT; 9 AA.  
AC P42998;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ANNETOCIN.  
OS Eisenia foetida (Common brandling worm) (Common dung-worm).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;  
OC Lumbricina; Lumbricidae; Eisenia.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=PITUITARY;  
RX MEDLINE=94121660; PubMed=8292046;  
RA Umi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,  
RA Nomoto K.;  
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,  
RT Eisenia foetida.;  
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).  
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO  
CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE  
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH  
CC NEPHRIDIAL FUNCTION.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR; PC2021; PC2021.  
DR INTERPRO: IPR000981; .  
DR PFAM: PF00220; hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
FT SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;  
SQ SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;  
Query Match 75.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 C 3  
DB 1 C 1  
RESULT 15  
OXYT\_OCTVU  
ID OXYT\_OCTVU STANDARD; PRT; 9 AA.  
AC P80027;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CEPHALOTOCIN.  
OS Octopus vulgaris (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;  
OC Incirrata; Octopodidae; Octopus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=NERVE ENDINGS;

RX MEDLINE=92270139; PubMed=1589145;  
 RA Reich G.;  
 RT "A new peptide of the oxytocin/vasopressin family isolated from  
 RL nerves of the cephalopod Octopus vulgaris.";  
 RL Neurosci. Lett. 134:191-194(1992).  
 CC -!- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA  
 CC CAVA.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR INTERPRO: IPR000981; -.  
 DR PFAM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9  
 SQ SEQUENCE 9 AA; 1072 MW; 17FF476B45409DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
 Db 1 C 1

Search completed: February 5, 2001, 12:06:02  
 Job time: 279 sec

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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:05:38 ; Search time 57.72 Seconds  
(without alignments)  
8.123 Million cell updates/sec

Title: US-09-687-267-5  
Perfect score: 12  
Sequence: 1 XXCX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL15:  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9	75.0	6	Q08720	Q08720 homo sapien
2	9	75.0	7	P70804	P70804 azotobacter
3	9	75.0	7	O55184	O55184 rattus norv
4	9	75.0	7	Q66113	Q66113 cherry leaf
5	9	75.0	7	Q67113	Q67113 influenza a
6	9	75.0	7	Q9YVE3	Q9YVE3 human adeno
7	9	75.0	7	Q9YVIR0	Q9YVIR0 human adeno
8	9	75.0	7	Q9YVIR0	Q9YVIR0 human adeno
9	9	75.0	7	Q9YVIR0	Q9YVIR0 human adeno
10	9	75.0	8	Q42564	Q42564 fugu rubrip
11	9	75.0	8	Q32560	Q32560 escherichia
12	9	75.0	8	Q15888	Q15888 homo sapien
13	9	75.0	8	Q15890	Q15890 homo sapien
14	9	75.0	8	Q15900	Q15900 homo sapien
15	9	75.0	8	Q9Y4X6	Q9Y4X6 homo sapien
16	9	75.0	8	Q02831	Q02831 oryctolagus
17	9	75.0	8	Q9YTR3	Q9YTR3 sus sp. ins
18	9	75.0	8	Q9SAY7	Q9SAY7 dioscorea t
19	9	75.0	8	P70243	P70243 mus musculu
					O35835 rattus norv

20	9	75.0	8	12	Q85562	Q85562 moloney mur
21	9	75.0	8	13	Q90493	Q90493 eopsaltia
22	9	75.0	8	13	Q90498	Q90498 erythrura g
23	9	75.0	8	13	Q91098	Q91098 manorina me
24	9	75.0	9	2	Q47063	Q47063 escherichia
25	9	75.0	9	4	O15999	O15999 homo sapien
26	9	75.0	9	4	Q99887	Q99887 homo sapien
27	9	75.0	9	6	Q9XT05	Q9XT05 macropus ru
28	9	75.0	9	6	Q9TUY0	Q9TUY0 monodelphis
29	9	75.0	9	9	Q38340	Q38340 lactococcus
30	9	75.0	9	11	Q9Q2A8	Q9Q2A8 mus musculu
31	9	75.0	9	11	P97889	P97889 rattus norv
32	9	75.0	9	12	Q69473	Q69473 human herpe
33	9	75.0	9	12	O12096	O12096 caprine art
34	9	75.0	9	12	O12098	O12098 caprine art
35	9	75.0	9	12	O12100	O12100 caprine art
36	9	75.0	9	12	O12102	O12102 caprine art
37	9	75.0	9	12	O12104	O12104 caprine art
38	9	75.0	9	12	O90350	O90350 hepatitis g
39	9	75.0	10	2	Q50032	Q50032 mycobacteri
40	9	75.0	10	2	Q47475	Q47475 escherichia
41	9	75.0	10	2	Q48469	Q48469 klebsiella
42	9	75.0	10	2	Q9K343	Q9K343 escherichia
43	9	75.0	10	3	Q9UW2	Q9UW2 schizophyll
44	9	75.0	10	4	Q13318	Q13318 homo sapien
45	9	75.0	10	4	Q9UN90	Q9UN90 homo sapien

ALIGNMENTS

RESULT 1  
ID Q08720 PRELIMINARY; PRT; 6 AA.  
AC Q08720;  
DT 01-NOV-1996 (TREMREL. 01, Created)  
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)  
DE Y PROTEIN (FRAGMENT).  
GN CREB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93010691; PubMed=1396344;  
RA Waeber G., Habener J.F.;  
RT "Novel testis germ cell-specific transcript of the CREB gene contains  
RT an alternatively spliced exon with multiple in-frame stop codons.";  
RL Endocrinology 131:2010-2015(1992).  
DR EMBL; X68994; CAA48780.1; -.  
FT NONTER 1 1  
FT NONTER 6 6  
SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
Db 4 C 4

RESULT 2  
ID P70804 PRELIMINARY; PRT; 7 AA.  
AC P70804;  
DT 01-FEB-1997 (TREMREL. 02, Created)  
DT 01-FEB-1997 (TREMREL. 02, Last sequence update)  
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)

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DE ALGG GENE (FRAGMENT).
GN
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
RN NCBI_TaxID=354;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
part of an alg gene cluster physically organized in a manner similar
to that in Pseudomonas aeruginosa.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A2D1AED0 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 1 C 1

RESULT 3
O55184 PRELIMINARY; PRT; 7 AA.
ID O55184;
AC O55184;
DT 01-JUN-1998 (TREMBlrel. 05, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ORPHAN RECEPTOR TR4-NS (FRAGMENT).
GN TR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
of novel sequences in the 5'-untranslated region and C-terminal
domain.";
RL Endocrinology 137:1562-1571(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299786; PubMed=8661150;
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
expression and chromosomal localization of the human gene.";
RL Genomics 35:361-366(1996).
DR EMBL; U59454; AAB91433.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 75.0%; Score 9; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 3 C 3

RESULT 4

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Q66113 PRELIMINARY; PRT; 7 AA.
ID Q66113;
AC Q66113;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE C-TERMINUS OF THE VIRAL REPLICASE (FRAGMENT).
OS Cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus.
OX NCBI_TaxID=12615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RA Borja M.;
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
strain).";
RL Virus Genes 10:245-252(1995).
DR EMBL; Z34265; CAA84019.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 4 C 4

RESULT 5
Q67113 PRELIMINARY; PRT; 7 AA.
ID Q67113;
AC Q67113;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE (UDORN/72) HEMAGGLUTININ (SEG 4) CDNA, 3' END (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922;
RA Dhar R., Chanock R.M., Lai C.J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 3 C 3

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RESULT 6
Q9YVE3 PRELIMINARY; PRT; 7 AA.
AC Q9YVE3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OC NCBI_TaxID=10519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GOMEN;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065065; AAD03662.1; -.
DR EMBL; AF065066; AAD03663.1; -.
FT NON_TER 1
FT SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 6 C 6

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RESULT 7
Q9YI90 PRELIMINARY; PRT; 7 AA.
AC Q9YI90;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7a.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OC NCBI_TaxID=85755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KN T96-0620, S-1058, CL 68578;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065068; AAD03668.1; -.
DR EMBL; AF065069; AAD03669.1; -.
DR EMBL; AF065067; AAD03666.1; -.
FT NON_TER 1
FT SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

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Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 6 C 6

RESULT 8
Q9YI09 PRELIMINARY; PRT; 7 AA.
AC Q9YI09;

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DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 4.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OC NCBI_TaxID=28280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2-G 95-873, RI-67, 55142;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03659.1; -.
DR EMBL; AF065062; AAD03653.1; -.
DR EMBL; AF065063; AAD03656.1; -.
FT NON_TER 1
FT SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

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Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 6 C 6

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RESULT 9
O42564 PRELIMINARY; PRT; 7 AA.
ID O42564;
AC O42564;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT (FRAGMENT).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OC NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
DR EMBL; U97673; AAB80916.1; -.
FT NON_TER 1
FT SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

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Query Match 75.0%; Score 9; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 5 C 5

RESULT 10
O32560 PRELIMINARY; PRT; 8 AA.
ID O32560;
AC O32560;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

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DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
DI PROPHONATE KINASE (FRAGMENT).  
GN TDCD.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W3110;  
RA Hesslinger C., Savers G.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
RL [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=W3110;  
RC Hesslinger C., Fairhurst S.A., Savers G.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ001820; CAA04875.1; -  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
DB 6 C 6

RESULT 11  
Q15888  
ID Q15888 PRELIMINARY; PRT; 8 AA.  
AC Q15888;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
DE (CLONE XP15H8A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32069; AAA73878.1; -  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
DB 5 C 5

RESULT 12  
Q15890  
ID Q15890 PRELIMINARY; PRT; 8 AA.  
AC Q15890;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)

DE (CLONE XP19G12A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32083; AAA73880.1; -  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
DB 4 C 4

RESULT 13  
Q15900  
ID Q15900 PRELIMINARY; PRT; 8 AA.  
AC Q15900;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
DE (CLONE XP7B11A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
RA Caskey C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32079; AAA73890.1; -  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAEB1 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
DB 2 C 2

RESULT 14  
Q9Y4X6  
ID Q9Y4X6 PRELIMINARY; PRT; 8 AA.  
AC Q9Y4X6;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE NUCLEAR LIM INTERACTOR (FRAGMENT).  
GN NLI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,  
 RA Schroth A., Bodem J., Royer-Pokora B.;  
 RT "Genomic structure, alternative transcripts and chromosomal  
 RT localization of the human LIM domain binding protein 1 gene  
 RT LDB1/NLI.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ243097; CAB45408.1; -;  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 767 MW; EE6EBDEB862D5B6 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
 |  
 Db 5 C 5

RESULT 15  
 O02831  
 ID O02831 PRELIMINARY; PRT; 8 AA.  
 AC O02831;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96377339; PubMed=8783186;  
 RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,  
 RA Vuorio E.;  
 RT "Evidence for insufficient chondrocytic differentiation during repair  
 RT of full-thickness defects of articular cartilage.";  
 RL Matrix Biol. 15:39-47(1996).  
 DR EMBL; S83371; AAD14433.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 75.0%; Score 9; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3  
 |  
 Db 4 C 4

Search completed: February 5, 2001, 12:05:38  
 Job time: 289 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:19 ; Search time 42.35 Seconds  
(without alignments)  
3.230 Million cell updates/sec

Title: US-09-687-267-6

Perfect score: 12  
Sequence: 1 XXXC 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_36.\*  
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
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19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	3	2 P10301	Sequence which cor
2	9	75.0	3	10 P90982	Binding receptor w
3	9	75.0	3	10 P91660	Synthetic peptide
4	9	75.0	3	14 R34022	Metal trapping pep
5	9	75.0	3	14 R34023	Metal trapping pep
6	9	75.0	3	15 R51439	IGF-1 analogue N-t
7	9	75.0	3	15 R51440	IGF-1 analogue N-t
8	9	75.0	3	15 R51441	IGF-1 analogue N-t
9	9	75.0	3	18 W19847	Human interleukin-
10	9	75.0	3	19 W56231	Anti-inflammatory
11	9	75.0	3	19 W56211	Anti-inflammatory
12	9	75.0	3	19 W56200	Anti-inflammatory

13	9	75.0	3	19 W56172	Anti-inflammatory
14	9	75.0	3	20 W80037	Peptide used in th
15	9	75.0	3	21 Y51896	Biostatin TR232 sy
16	9	75.0	4	2 P10138	Sequence of antiin
17	9	75.0	4	2 P10093	Sequence of peptid
18	9	75.0	4	2 P10382	Enkephalin-like an
19	9	75.0	4	3 P20217	Analgesic and neur
20	9	75.0	4	4 P30083	Sequence of chromo
21	9	75.0	4	4 P30085	Sequence of chromo
22	9	75.0	4	5 P40538	Sequence of cyclic
23	9	75.0	4	5 P40539	Sequence of cyclic
24	9	75.0	4	8 P70833	Sequence encoded b
25	9	75.0	4	10 P91661	Synthetic peptide
26	9	75.0	4	12 R11077	Peptide fragment #
27	9	75.0	4	12 R11079	Peptide fragment #
28	9	75.0	4	12 R11508	Thioredoxin active
29	9	75.0	4	12 R11744	Cyclic platelet ag
30	9	75.0	4	12 R11745	Cyclic platelet ag
31	9	75.0	4	12 R12554	Ocular pressure re
32	9	75.0	4	12 R13935	Antibiotic FR90137
33	9	75.0	4	12 R14723	Farnesyl-protein t
34	9	75.0	4	12 R15751	Farnesyl-protein t
35	9	75.0	4	12 R15752	Farnesyl-protein t
36	9	75.0	4	12 R15753	Farnesyl-protein t
37	9	75.0	4	12 R15754	Farnesyl-protein t
38	9	75.0	4	12 R15755	Farnesyl-protein t
39	9	75.0	4	12 R15756	Farnesyl-protein t
40	9	75.0	4	12 R15757	Farnesyl-protein t
41	9	75.0	4	12 R15758	Farnesyl-protein t
42	9	75.0	4	12 R15759	Farnesyl-protein t
43	9	75.0	4	12 R15760	Farnesyl-protein t
44	9	75.0	4	12 R15761	Farnesyl-protein t
45	9	75.0	4	21 Y80840	Fluorophore-label

ALIGNMENTS

RESULT 1  
P10301  
ID P10301 standard; Protein; 3 AA.  
AC P10301;  
DT 19-AUG-1992 (first entry)  
XX Sequence which corresp. to residues 19-21 of insulin A chain.  
DE Cystine peptide; insulin activity; hormone; diabetes therapy;  
KW antidiabetic agent.  
KW Mammal.  
OS Key Location/Qualifiers  
FH Disulfide-bond 2 /note= "bonded to Cys(5) of P10115, which is  
FT residue 19 of the B chain fragment  
FT B15-27"  
XX DD147942-A.  
XX 29-APR-1981.  
XX 01-FEB-1980; 80DD-0011868.  
XX 20-AUG-1979; 79DD-0215100.  
XX (LOSS)/ LOSSE G.  
XX Losse G, Stange H;  
XX Anti-inflammatory  
XX WPI; 1981-53498D/30 (53498D).

PT Cysteine peptide(s) with antidiabetic activity - contg. fragments  
 XX of insulin A and B chains

XX Claim 1; Page 10; 11pp; German.

XX The inventors claim the prepn. of new cysteine peptides with insulin-  
 CC like activity. The new peptides comprise a sequence with corresp. to  
 CC a central portion of the insulin B chain (esp. B15-27) and a  
 CC cysteine-contg. peptide with an AA sequence corresp. to a terminal  
 CC portion of the insulin A chain (esp. A1-7). The new cysteine  
 CC peptides are antidiabetic agents with appreciable insulin activity  
 CC (lower than that of insulin itself) and low antigenic activity.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
 |  
 Db 2 c 2

RESULT 2

ID P90982 standard; peptide; 3 AA.

AC P90982;

DT 06-JUN-1990 (first entry)

XX Binding receptor with selectivity for a target ligand, borne by  
 DE an article for inactivating toxic materials.

XX Toxic material; inactivator; organophosphorous cpds.; nerve poison;  
 KW pesticide; decontaminant; military.

XX WO8902920-A.

XX 06-APR-1989.

XX 04-OCT-1988; 88WO-US03422.

XX 05-OCT-1987; 87US-0105312.

XX (LITT ) LITTLE AD INC.

XX Taylor RF;

XX WPI; 1989-114395/15.

XX Article for inactivating toxic materials, eg organo:phosphorous cpds. -  
 PT comprises solid carrier bearing target ligand binding receptor  
 PT and ligand-degrading receptor, pref. enzyme

XX Claim 7a; page 42; 57pp; English.

XX The article for inactivating a toxic material comprises a solid carrier  
 CC bearing a first receptor which binds the target ligand and a second  
 CC receptor which degrades the target ligand. This synthetic peptide is  
 CC a preferred first receptor. The article may be used for covering  
 CC surfaces to protect or decontaminate the surface. The article is esp. for  
 CC degrading toxic organic cpds., esp. organophosphorous cpds., (eg  
 CC pesticides and nerve poisons, bacteria and viruses, in environmental,  
 CC chemical, military and industrial settings.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
 |  
 Db 2 c 2

RESULT 3

ID P91660 standard; protein; 3 AA.

XX P91660;

AC P91660;

XX 29-JUN-1990 (first entry)

XX Synthetic peptide corresp. to residues 12-14 of naturally occurring

DE epidermal growth factor (EGF).

XX Epidermal growth factor; angiogenesis; synthetic peptide.

XX Key :Location/Qualifiers

FT Misc-difference 1

FT ./label=OTHER

FT ./note="H-Gly"

FT Misc-difference 3

FT ./label=OTHER

FT ./note="(aceto amido methyl) NH2-Cys"

XX WO8901489-A.

XX 23-FEB-1989.

XX 10-AUG-1988; 88WO-AU00300.

XX 10-AUG-1987; 87AU-0003629.

XX (CSIR ) COMMONWEALTH SCIENT ORG.

XX McAuslan BR;

XX WPI; 1989-068852/09.

XX Synthetic peptide active in stimulating angiogenesis -  
 PT has sequences corresponding to amino acid sequences occurring in  
 PT epidermal growth factor.

XX Claim 3; page 10; 11pp; English.

XX The inventors claim synthetic peptides which correspond to sequences  
 CC occurring in EGF, but excluding EGF. The peptides are angiogenic  
 CC and have corresp. applications, eg for the healing of wounds and  
 CC burns. Their relative shortness means that they pose fewer synthesis  
 CC problems than the entire EGF molecule. They can be admin. singly or  
 CC association with each other or in association with an angiogenic  
 CC stimulator.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
 |  
 Db 3 c 3

RESULT 4

ID R34022 standard; peptide; 3 AA.

XX R34022;

AC R34022;

XX 19-MAY-1993 (first entry)  
XX Metal trapping peptide intermediate.  
XX Electrostatic interaction; metalloprotein; binding site;  
KW protecting group.  
XX Synthetic.  
XX OS  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Boc protected"  
FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH  
FT of cysteine"  
FT Modified-site 3 /note= "OMe protected"  
XX JP04346999-A.  
XX 02-DEC-1992.  
XX 24-MAY-1991; 91JP-0120196.  
XX 24-MAY-1991; 91JP-0120196.  
XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.  
XX WPI; 1993-021449/03.  
XX New acyclic peptide with metal trapping activity - exhibits in  
PT vivo metal transporting action and can be used as drug,  
PT diagnostic agent or functional material  
XX Claim 3; Page 2; 9pp; Japanese.  
XX The acyclic peptide (see R31340) with metal trapping activity may be  
CC produced by fragment condensation using the peptide fragments given in  
CC R34022-29.  
XX Sequence 3 AA;  
SQ  
Query Match 75.0%; Score 9; DB 14; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 C 4  
Db 2 c 2  
RESULT 5  
R34023  
ID R34023 standard; peptide; 3 AA.  
XX AC R34023;  
XX 19-MAY-1993 (first entry)  
XX Metal trapping peptide intermediate.  
XX Electrostatic interaction; metalloprotein; binding site;  
KW protecting group.  
XX Synthetic.  
XX OS  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "HCl.H-Val"  
FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH

FT Modified-site 3 /note= "OMe protected"  
FT of cysteine"  
XX JP04346999-A.  
XX 02-DEC-1992.  
XX 24-MAY-1991; 91JP-0120196.  
XX 24-MAY-1991; 91JP-0120196.  
XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.  
XX WPI; 1993-021449/03.  
XX New acyclic peptide with metal trapping activity - exhibits in  
PT vivo metal transporting action and can be used as drug,  
PT diagnostic agent or functional material  
XX Claim 3; Page 2; 9pp; Japanese.  
XX The acyclic peptide (see R31340) with metal trapping activity may be  
CC produced by fragment condensation using the peptide fragments given in  
CC R34022-29.  
XX Sequence 3 AA;  
SQ  
Query Match 75.0%; Score 9; DB 14; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 C 4  
Db 2 c 2  
RESULT 6  
R51439  
ID R51439 standard; peptide; 3 AA.  
XX AC R51439;  
XX 27-OCT-1994 (first entry)  
XX IGF-1 analogue N-terminal.  
XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;  
KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.  
XX Homo sapiens.  
XX WO9406445-A.  
XX 31-MAR-1994.  
XX 02-SEP-1993; 93WO-US08279.  
XX 17-SEP-1992; 92US-0947035.  
XX (EMBR-) EMBREX INC.  
XX (GROP-) GROPEP PTY LTD.  
XX (USDA) US SEC OF AGRIC.  
XX Ballard FJ, Francis GL, McMurtry JP, Phelps PV;  
PI Walton PE;  
XX WPI; 1994-118144/14.  
XX Increasing growth of birds - with insulin-like growth factor  
PT delivered to the egg before hatching esp. for increasing wt. gain  
PT in chickens.

XX Claim 6; Page 37; 45pp; English.

XX Growth of birds is increased by (a) admin. to the bird, in ovo,

CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;

CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.

CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or

CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,

CC partic. Gly and the Thr normally adjacent to Glu can be replaced

CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal

CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced

CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent

CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.

CC comprises the N-terminal given in R51450-53.

CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human

CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid

CC N-terminal extension.

XX Sequence 3 AA;

SQ

Query Match 75.0%; Score 9; DB 15; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4

Db 3 C 3

RESULT 7

R51440

ID R51440 standard; peptide; 3 AA.

XX

AC R51440;

XX

DT 27-OCT-1994 (first entry)

XX

DE IGF-1 analogue N-terminal.

XX

KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;

KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.

XX

OS Homo sapiens.

XX

PN W09406445-A.

XX

PD 31-MAR-1994.

XX

PF 02-SEP-1993; 93WO-US08279.

XX

PR 17-SEP-1992; 92US-0947035.

XX

PA (EMBR-) EMBREX INC.

PA (GROP-) GROPEP PTY. LTD.

PA (USDA) US SEC OF AGRIC.

XX

PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;

PI Walton PE;

XX

DR WPI; 1994-118144/14.

XX

XX Increasing growth of birds - with insulin-like growth factor

PT delivered to the egg before hatching esp. for increasing wt. gain

PT in chickens.

XX

PS Claim 6; Page 37; 45pp; English.

XX

CC Growth of birds is increased by (a) admin. to the bird, in ovo,

CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;

CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.

CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or

CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,

CC partic. Gly and the Thr normally adjacent to Glu can be replaced

CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal

CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced

CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent

CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.

CC comprises the N-terminal given in R51450-53.

CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human

CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid

CC N-terminal extension.

XX Sequence 3 AA;

SQ

Query Match 75.0%; Score 9; DB 15; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4

Db 3 C 3

RESULT 8

R51441

ID R51441 standard; peptide; 3 AA.

XX

AC R51441;

XX

DT 27-OCT-1994 (first entry)

XX

DE IGF-1 analogue N-terminal.

XX

KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;

KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.

XX

OS Homo sapiens.

XX

PN W09406445-A.

XX

PD 31-MAR-1994.

XX

PF 02-SEP-1993; 93WO-US08279.

XX

PR 17-SEP-1992; 92US-0947035.

XX

PA (EMBR-) EMBREX INC.

PA (GROP-) GROPEP PTY. LTD.

PA (USDA) US SEC OF AGRIC.

XX

PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;

PI Walton PE;

XX

DR WPI; 1994-118144/14.

XX

XX Increasing growth of birds - with insulin-like growth factor

PT delivered to the egg before hatching esp. for increasing wt. gain

PT in chickens.

XX

PS Claim 6; Page 37; 45pp; English.

XX

CC Growth of birds is increased by (a) admin. to the bird, in ovo,

CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;

CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.

CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or

CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,

CC partic. Gly and the Thr normally adjacent to Glu can be replaced

CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal

CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced  
 CC by Gly, Glu, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent  
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.  
 CC comprises the N-terminal given in R51450-53.  
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human  
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid  
 CC N-terminal extension.  
 XX  
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 15; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 |  
 Db 3 C 3

## RESULT 9

W19847  
 ID W19847 standard; Peptide; 3 AA.  
 AC W19847;

XX 23-SEP-1997 (first entry)

XX Human interleukin-12 p40 subunit N-terminal peptide.

XX Interleukin-12; Fc gamma-1; immunosuppressive; autoimmune disease;  
 KW graft rejection; toxic shock; therapy.  
 XX Homo sapiens.

OS

XX WO9720062-A1.

PN 05-JUN-1997.

XX 02-DEC-1996; 96WO-US19181.

PF 01-DEC-1995; 95US-0565856.

XX (BETH-) BETH ISRAEL HOSPITAL ASSOC.

PA (UYMA-) UNIV MASSACHUSETTS.

PI Steel AW, Strom TB;

XX WPI; 1997-310615/28.

DR N-PSDB; T72095-96.

XX Fusion protein containing interleukin-12 p40 sub-unit - has  
 PT increased stability, used to inhibit graft rejection, or treat  
 PT autoimmune disease and endotoxin-induced shock

XX Example; Fig 2; 36pp; English.

XX A peptide (W19847) comprises the three N-terminal amino acid  
 CC residues of human interleukin-12 (IL-12) p40 subunit. It is  
 CC encoded both by native human p40 cDNA (T72096) and by a primer  
 CC (T72095) based on the native sequence. PCR amplification has  
 CC been used to amplify p40 cDNA. A fusion protein comprising the  
 CC p40 subunit and human Fc gamma-1 (see also W19853) was expressed  
 CC in E. coli. This fusion protein has a longer in vivo half-life  
 CC than native p40 and can be used as an immunosuppressive (e.g. to  
 CC treat autoimmune diseases or to inhibit graft rejection) or to  
 CC treat or prevent endotoxin-induced shock.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 18; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 C 4  
 |  
 Db 2 C 2

## RESULT 10

W56231  
 ID W56231 standard; peptide; 3 AA.  
 AC W56231;

XX 20-JUL-1998 (first entry)

XX Anti-inflammatory tripeptide.

XX

KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;  
 KW T-cell inhibitory activity; adherence; extracellular matrix;  
 KW up-regulation; fas receptor expression; inflammation.

XX Synthetic.

XX WO9809985-A2.

XX 12-MAR-1998.

XX 03-SEP-1997; 97WO-IL00295.

XX 28-MAY-1997; 97US-0864301.

PR 03-SEP-1996; 96US-0025376.

PR 20-NOV-1996; 96US-0753141.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Beserman P, Eisenbachschwartz M, Hirschberg DL;

XX WPI; 1998-193550/17.

XX Anti-inflammatory peptides and derivatives - used for treating, e.g.  
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,  
 PT shock, HIV infection, transplant rejection or Alzheimer's disease

XX Claim 7; Page 35; 42pp; English.

XX W56171-248 represent anti-inflammatory tripeptides of the invention.  
 CC They are derived from the formulae:

CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where

CC Xaa = any amino acid residue.

CC Cyclic derivatives of the peptides also function as anti-inflammatory  
 CC agents. The peptides can be covalently linked to one another either  
 CC directly or through a spacer. The peptides and their derivatives have  
 CC macrophage inhibitory and T-cell inhibitory activity and thus,  
 CC anti-inflammatory activity. The peptides and compositions have  
 CC anti-immune activity, i.e. inhibitory effects against a cellular and  
 CC humoral immune response, including a response not associated with  
 CC inflammation. The peptides also inhibit the ability of macrophages and  
 CC T-cells to adhere to extracellular matrix components and fibronectin, as  
 CC well as up-regulated fas receptor expression in T-cells. They can be used  
 CC to inhibit unwanted immune reaction and inflammation.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
 |  
 Db 3 C 3

```

RESULT 11
ID W56211 standard; peptide; 3 AA.
XX AC W56211;
XX DT 20-JUL-1998 (first entry)
XX DE Anti-inflammatory tripeptide.
XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX OS Synthetic.
XX PN WO9809985-A2.
XX PR 03-SEP-1997; 97WO-IL00295.
XX PR 28-MAY-1997; 97US-0864301.
XX PR 03-SEP-1996; 96US-0025376.
XX PR 20-NOV-1996; 96US-0753141.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX DR WPI; 1998-193550/17.
XX DT Anti-inflammatory peptides and derivatives - used for treating, e.g.
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
PT shock, HIV infection, transplant rejection or Alzheimer's disease
XX PS Claim 6; Page 35; 42pp; English.
XX CC W56171-248 represent anti-inflammatory tripeptides of the invention.
CC They are derived from the formulae:
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
CC Xaa = any amino acid residue.
CC Cyclic derivatives of the peptides also function as anti-inflammatory
CC agents. The peptides can be covalently linked to one another either
CC directly or through a spacer. The peptides and their derivatives have
CC macrophage inhibitory and T-cell inhibitory activity and thus,
CC anti-inflammatory activity. The peptides and compositions have
CC anti-immune activity, i.e. inhibitory effects against a cellular and
CC humoral immune response, including a response not associated with
CC inflammation. The peptides also inhibit the ability of macrophages and
CC T-cells to adhere to extracellular matrix components and fibronectin, as
CC well as up-regulated fas receptor expression in T-cells. They can be used
CC to inhibit unwanted immune reaction and inflammation.
XX SQ Sequence 3 AA;
Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 C 4
DB 1 C 1
RESULT 12
ID W56200 standard; peptide; 3 AA.
XX AC W56200;
XX DT 20-JUL-1998 (first entry)

```

```

XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX OS Synthetic.
XX PN WO9809985-A2.
XX PD 12-MAR-1998.
XX PF 03-SEP-1997; 97WO-IL00295.
XX PR 28-MAY-1997; 97US-0864301.
XX PR 03-SEP-1996; 96US-0025376.
XX PR 20-NOV-1996; 96US-0753141.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX DR WPI; 1998-193550/17.
XX DT Anti-inflammatory peptides and derivatives - used for treating, e.g.
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
PT shock, HIV infection, transplant rejection or Alzheimer's disease
XX PS Claim 5; Page 34; 42pp; English.
XX CC W56171-248 represent anti-inflammatory tripeptides of the invention.
CC They are derived from the formulae:
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
CC Xaa = any amino acid residue.
CC Cyclic derivatives of the peptides also function as anti-inflammatory
CC agents. The peptides can be covalently linked to one another either
CC directly or through a spacer. The peptides and their derivatives have
CC macrophage inhibitory and T-cell inhibitory activity and thus,
CC anti-inflammatory activity. The peptides and compositions have
CC anti-immune activity, i.e. inhibitory effects against a cellular and
CC humoral immune response, including a response not associated with
CC inflammation. The peptides also inhibit the ability of macrophages and
CC T-cells to adhere to extracellular matrix components and fibronectin, as
CC well as up-regulated fas receptor expression in T-cells. They can be used
CC to inhibit unwanted immune reaction and inflammation.
XX SQ Sequence 3 AA;
Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 C 4
DB 3 C 3
RESULT 13
ID W56172 standard; peptide; 3 AA.
XX AC W56172;
XX DT 20-JUL-1998 (first entry)
XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX

```

OS Synthetic.  
 PN WO9809985-A2.  
 XX  
 PD 12-MAR-1998.  
 XX  
 PF 03-SEP-1997; 97WO-IL00295.  
 XX  
 PR 28-MAY-1997; 97US-0864301.  
 PR 03-SEP-1996; 96US-0025376.  
 PR 20-NOV-1996; 96US-0753141.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Beserman P, Eisenbachschwartz M, Hirschberg DL;  
 XX WPI; 1998-193550/17.  
 DR  
 XX  
 XX Anti-inflammatory peptides and derivatives - used for treating, e.g.  
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,  
 PT shock, HIV infection, transplant rejection or Alzheimer's disease  
 XX  
 PS Claim 3; Page 34; 42pp; English.  
 XX  
 CC W56171-248 represent anti-inflammatory tripeptides of the invention.  
 CC They are derived from the formulae:  
 CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where  
 CC Xaa = any amino acid residue.  
 CC Cyclic derivatives of the peptides also function as anti-inflammatory  
 CC agents. The peptides can be covalently linked to one another either  
 CC directly or through a spacer. The peptides and their derivatives have  
 CC macrophage inhibitory and T-cell inhibitory activity and thus,  
 CC anti-inflammatory activity. The peptides and compositions have  
 CC anti-immune activity, i.e. inhibitory effects against a cellular and  
 CC humoral immune response, including a response not associated with  
 CC inflammation. The peptides also inhibit the ability of macrophages and  
 CC T-cells to adhere to extracellular matrix components and fibronectin, as  
 CC well as up-regulated fas receptor expression in T-cells. They can be used  
 CC to inhibit unwanted immune reaction and inflammation.  
 XX  
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
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 Db 1 c 1

RESULT 14  
 W88037  
 ID W88037 standard; peptide; 3 AA.  
 AC W88037;  
 XX  
 DT 09-APR-1999 (first entry)  
 XX  
 DE Peptide used in the hair composition of the invention.  
 XX  
 KW Hair; styling; wave.  
 XX  
 OS Synthetic.  
 XX  
 PN JP11012138-A.  
 XX  
 PD 19-JAN-1999.  
 XX  
 PF 18-JUN-1997; 97JP-0161657.  
 XX

PR 18-JUN-1997; 97JP-0161657.  
 XX (LIOY ) LION CORP.  
 XX  
 DR WPI; 1999-148442/13.  
 XX  
 PT New composition for hair - comprises oligopeptide having more than 2  
 PT cysteine residues and reducing agent  
 XX  
 PS Example 2; Page 6; 17pp; Japanese.  
 XX  
 CC Peptides W88033-39 are used in the hair composition of the invention.  
 CC The specification describes a hair composition that comprises at  
 CC least one oligopeptide having more than two cysteine residues and more  
 CC than three amino acid residues of the same kind (except cysteine) and a  
 CC reducing agent. The composition is useful for styling hair to take  
 CC various shapes and waves safely and effectively.  
 XX  
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 20; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
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 Db 1 c 1

RESULT 15  
 Y51896  
 ID Y51896 standard; peptide; 3 AA.  
 XX  
 AC Y51896;  
 XX  
 DT 16-JUN-2000 (first entry)  
 XX  
 DE Biostatin TT232 synthesising peptide 1.  
 XX  
 KW Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor;  
 KW cellular proliferation inhibition; somatostatin; antitumor.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FH Modified-site 1 /note= "TFA\*Lys(z)"  
 FT Modified-site 2  
 FT Modified-site 3 /note= "Cys(Acm)"  
 FT Modified-site /note= "Thr(tBu) with C-terminal amide group"  
 XX  
 PN WO200011032-A2.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-EP06131.  
 XX  
 PR 20-AUG-1998; 98WO-EP05306.  
 XX  
 PA (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.  
 XX  
 PI Braum G, Lifferth A, Birr C;  
 XX WPI; 2000-224663/19.  
 DR  
 XX Biostatin preparation in high yield by solid synthesis, including  
 PT closure of disulfide bridge before cleavage from support, useful as  
 PT antitumor agent  
 XX  
 PS Example 4; Page 23; 33pp; German.  
 XX

CC This invention describes a novel method for the solid phase (SP)  
CC synthesis of biostatin (TT 232) (I) which includes closing the disulfide  
CC bridge by oxidation of the completely or partially constructed peptide  
CC while still bonded to the solid phase. The products of the invention have  
CC cytostatic activity and are tyrosine kinase inhibitors. (I) inhibits the  
CC tyrosine kinase activity of various human stomach cancer cell lines and  
CC thus inhibits cellular proliferation. The heptapeptide (I) described in  
CC the invention is a somatostatin analog which shows strong antitumor  
CC activity in vitro and in vivo. The SP synthesis method gives (I) is more  
CC easily and in markedly higher yield than by the method of EP505680, in  
CC which the cyclization is carried out after cleaving the peptide from the  
CC resin. The solution method is also a simple synthesis of (I) in high  
CC yield; typically the tert-butyl-protected precursor can be oxidized in  
CC a yield of 70-80%. Y51896-Y51900 represent peptides used in the  
CC synthesis of biostatin TT232 described in the method of the invention.

XX

SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 21; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4  
Db 2 c 2

Search completed: February 5, 2001, 12:01:19  
Job time: 366 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:54 ; Search time 30.91 Seconds  
(without alignments)  
2.324 Million cell updates/sec

Title: US-09-687-267-6

Perfect score: 12

Sequence: 1 XXXC 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*

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4: /cgn2\_6/ptodata/2/iaa/PTCUS\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	2	1 US-07-791-213D-23	Sequence 23, Appl
2	9	75.0	2	1 US-07-791-213D-39	Sequence 39, Appl
3	9	75.0	2	1 US-08-133-804-9	Sequence 9, Appl
4	9	75.0	2	1 US-08-354-240A-12	Sequence 12, Appl
5	9	75.0	2	1 US-08-461-838-9	Sequence 9, Appl
6	9	75.0	2	1 US-08-293-150A-23	Sequence 23, Appl
7	9	75.0	2	1 US-08-293-150A-39	Sequence 39, Appl
8	9	75.0	2	2 US-08-461-886-9	Sequence 9, Appl
9	9	75.0	2	2 US-08-465-380-307	Sequence 307, App
10	9	75.0	2	2 US-08-486-397-307	Sequence 307, App
11	9	75.0	2	2 US-08-486-399-307	Sequence 307, App
12	9	75.0	2	2 US-08-461-965-307	Sequence 307, App
13	9	75.0	2	2 US-08-634-641-307	Sequence 307, App
14	9	75.0	2	2 US-08-818-253-52	Sequence 52, Appl
15	9	75.0	2	3 US-09-249-471-307	Sequence 307, App
16	9	75.0	2	3 US-09-249-472-307	Sequence 307, App
17	9	75.0	2	3 US-09-249-451-307	Sequence 307, App
18	9	75.0	2	3 US-08-809-455-307	Sequence 307, App
19	9	75.0	2	3 US-09-249-461-307	Sequence 307, App
20	9	75.0	2	3 US-09-249-448-307	Sequence 307, App
21	9	75.0	2	3 US-07-791-213D-22	Sequence 22, Appl
22	9	75.0	3	1 US-07-791-213D-38	Sequence 38, Appl
23	9	75.0	3	1 US-07-945-982-2	Sequence 2, Appl
24	9	75.0	3	1 US-07-945-982-8	Sequence 8, Appl
25	9	75.0	3	1 US-07-947-035-3	Sequence 3, Appl
26	9	75.0	3	1 US-07-947-035-4	Sequence 4, Appl
27	9	75.0	3	1 US-07-947-035-5	Sequence 5, Appl
28	9	75.0	3	1 US-08-285-443-4	Sequence 4, Appl

29 9 75.0 3 1 US-08-079-812-31 Sequence 31, Appl  
30 9 75.0 3 1 US-08-122-510-11 Sequence 11, Appl  
31 9 75.0 3 1 US-08-122-510-12 Sequence 12, Appl  
32 9 75.0 3 1 US-08-122-510-13 Sequence 13, Appl  
33 9 75.0 3 1 US-07-789-913-26 Sequence 26, Appl  
34 9 75.0 3 1 US-08-371-930-4 Sequence 4, Appl  
35 9 75.0 3 1 US-08-049-794-26 Sequence 26, Appl  
36 9 75.0 3 1 US-08-372-455-2 Sequence 2, Appl  
37 9 75.0 3 1 US-08-372-455-8 Sequence 8, Appl  
38 9 75.0 3 1 US-08-321-585A-1 Sequence 1, Appl  
39 9 75.0 3 1 US-08-321-585A-2 Sequence 2, Appl  
40 9 75.0 3 1 US-08-321-585A-3 Sequence 3, Appl  
41 9 75.0 3 1 US-08-446-908-14 Sequence 14, Appl  
42 9 75.0 3 1 US-08-231-205A-14 Sequence 14, Appl  
43 9 75.0 3 1 US-08-293-150A-22 Sequence 22, Appl  
44 9 75.0 3 1 US-08-293-150A-38 Sequence 38, Appl  
45 9 75.0 3 3 US-08-447-515-12 Sequence 12, Appl

#### ALIGNMENTS

RESULT 1

US-07-791-213D-23

; Sequence 23, Application US/07791213D

; Patent No. 5409895

; GENERAL INFORMATION:

; APPLICANT: MORISHITA, Hideaki

; APPLICANT: KANAMORI, Toshihiko

; APPLICANT: NOBUHARA, Masahiro

; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE

; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME

; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF

; TITLE OF INVENTION: TREATING USING THE SAME

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P. O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07791,213D

; FILING DATE: 13-NOV-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 2-306745

; FILING DATE: 13-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 029650-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-07-791-213D-23

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 C 4
       1
Db      2 C 2

RESULT  2
US-07-791-213D-39
; Sequence 39, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: KANAMORI, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-39

Query Match      75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 C 4
       1
Db      1 C 1

RESULT  3
US-08-133-804-9
; Sequence 9, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/133,804
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..2
; OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
US-08-133-804-9

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 C 4
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Db      2 C 2

RESULT  4
US-08-354-240A-12
; Sequence 12, Application US/08354240A
; Patent No. 5670356
; GENERAL INFORMATION:
; APPLICANT: Sherif, Bruce A.
; APPLICANT: Wood, Keith V.
; TITLE OF INVENTION: MODIFIED LUCIFERASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,240A
; FILING DATE: 12-DEC-1994
; CLASSIFICATION: 435
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ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 34506.029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-831-2100  
TELEFAX: 608-831-2106  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-354-240A-12

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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 C 1

RESULT 5  
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; Sequence 9, Application US/08461838  
; Patent No. 5753204  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For  
; TITLE OF INVENTION: Imaging  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/461,838  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kelley, Robin D.  
; REGISTRATION NUMBER: 34,637  
; REFERENCE/DOCKET NUMBER: 2054/22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7477  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
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; LOCATION: 1..2  
; OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"  
US-08-461-838-9

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
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Db 2 C 2

RESULT 6  
US-08-293-150A-23  
; Sequence 23, Application US/08293150A  
; Patent No. 5792629  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,150A  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,213  
; FILING DATE: 13-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-049  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-293-150A-23

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
|  
Db 2 C 2

RESULT 7  
US-08-293-150A-39  
; Sequence 39, Application US/08293150A

Patent No. 5792629  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TITLE OF INVENTION: TREATING USING THE SAME  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293.150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-293-150A-39

Query Match 75.0%; Score 9; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
Db 1 C 1

RESULT 8  
US-08-461-386-9  
Sequence 9, Application US/08461386  
Patent No. 5837846  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
TITLE OF INVENTION: Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston

STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461.386  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..2  
OTHER INFORMATION: /note= "C-terminal Tail (Ser-Cys)"  
US-08-461-386-9

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
Db 2 C 2

RESULT 9  
US-08-465-380-307  
Sequence 307, Application US/08465380  
Patent No. 5863894  
GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465.380  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/268  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.  
US-08-465-380-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 C 4  
|  
Db 1 C 1

RESULT 10  
US-08-486-397-307  
;; Sequence 307, Application US/08486397  
;; Patent No. 5866542  
;; GENERAL INFORMATION:  
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
;; APPLICANT: Peter W. Bergum  
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
;; TITLE OF INVENTION: PROTEIN  
;; NUMBER OF SEQUENCES: 357  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; STREET: Suite 4700  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/486,397  
;; FILING DATE: June 5, 1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/269  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.  
US-08-486-397-307  
  
Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 C 4  
|  
Db 1 C 1

RESULT 11  
US-08-486-399-307  
;; Sequence 307, Application US/08486399  
;; Patent No. 5866543  
;; GENERAL INFORMATION:  
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
;; APPLICANT: Peter W. Bergum  
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
;; TITLE OF INVENTION: PROTEIN  
;; NUMBER OF SEQUENCES: 356  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; STREET: Suite 4700  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/486,399  
;; FILING DATE: June 5, 1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 213/270  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 307:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; FRAGMENT TYPE: internal fragment  
;; FEATURE:  
;; OTHER INFORMATION: Xaa in location 2 is an  
;; amino acid.

US-08-486-399-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
|  
Db 1 C 1

## RESULT 12

US-08-461-965-307  
; Sequence 307, Application US/08461965  
; Patent No. 5872098  
; GENERAL INFORMATION:  
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
; APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,  
; APPLICANT: Peter W. Bergum  
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,965  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 210/243  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; OTHER INFORMATION: amino acid.

US-08-461-965-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4  
|  
Db 1 C 1

## RESULT 13

US-08-634-641-307  
; Sequence 307, Application US/08634641  
; Patent No. 5955294  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George P. Vlasuk  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Mensens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Ganssemans, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew  
; APPLICANT: Bergum, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/634,641  
; FILING DATE: April 19, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13231  
; FILING DATE: October 17, 1995  
; APPLICATION NUMBER: 08/486,399  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/486,397  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/465,380  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/461,965  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 219/136  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; OTHER INFORMATION: amino acid.

US-08-634-641-307

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 C 4  
Db 1 C 1

## RESULT 14

US-08-818-253-52  
; Sequence 52, Application US/08818253  
; Patent No. 5998204  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Miyawaki, Atsushi  
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
; DETECTION OF ANALYTES  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,253  
; FILING DATE: 14-MAR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halle, Ph.D., Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07257/043001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-818-253-52

Query Match 75.0%; Score 9; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 C 4  
Db 1 C 1

## RESULT 15

US-09-249-471-307  
; Sequence 307, Application US/09249471  
; Patent No. 604041  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George Phillip  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Messens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Ganssemans, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew  
; APPLICANT: Berghum, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/249,471  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/809,455  
; FILING DATE: April 17, 1997  
; APPLICATION NUMBER: PCT/US95/13231  
; FILING DATE: October 17, 1995  
; APPLICATION NUMBER: 08/486,399  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/486,397  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/465,380  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/461,965  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 216/270  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 307:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal fragment  
; FEATURE:  
; OTHER INFORMATION: Xaa in location 2 is an  
; OTHER INFORMATION: amino acid.  
US-09-249-471-307

Query Match 75.0%; Score 9; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 C 4  
Db 1 C 1

Search completed: February 5, 2001, 12:01:54  
Job time: 336 sec

